

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 18, 2004, 05:09:18 ; Search time 746.333 Seconds  
(without alignments)  
1684.164 Million cell updates/sec

Title: US-09-310-844C-25

Perfect score: 29  
Sequence: 1 aaagaucuuuuuuuaagccccaagggcu 29

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 1774092

Minimum DB seq length: 0  
Maximum DB seq length: 80

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database :

GenEmbl:

- 1: gb.ba.\*
- 2: gb.htg.\*
- 3: gb.in.\*
- 4: gb.om.\*
- 5: gb.ov.\*
- 6: gb.pat.\*
- 7: gb.ph.\*
- 8: gb.pl.\*
- 9: gb.pr.\*
- 10: gb.ro.\*
- 11: gb.sts.\*
- 12: gb.sy.\*
- 13: gb.un.\*
- 14: gb.vi.\*
- 15: em.ba.\*
- 16: em.fun.\*
- 17: em.hum.\*
- 18: em.in.\*
- 19: em.mu.\*
- 20: em.om.\*
- 21: em.or.\*
- 22: em.ov.\*
- 23: em.pat.\*
- 24: em.ph.\*
- 25: em.pl.\*
- 26: em.ro.\*
- 27: em.sts.\*
- 28: em.un.\*
- 29: em.vi.\*
- 30: em.htg.hum.\*
- 31: em.htg.inv.\*
- 32: em.htg.other.\*
- 33: em.htg.mus.\*
- 34: em.htg.pln.\*
- 35: em.htg.rtd.\*
- 36: em.htg.nam.\*
- 37: em.htg.vrt.\*
- 38: em.sy.\*
- 39: em.htgo.hum.\*
- 40: em.htgo.mus.\*
- 41: em.htgo.other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | DB | ID        | Description        |
|------------|-------|---------------|--------|----|-----------|--------------------|
| 1          | 29    | 100.0         | 42     | 6  | BD274272  | BD274272 Identific |
| 2          | 29    | 100.0         | 42     | 6  | BD274273  | BD274273 Identific |
| 3          | 29    | 100.0         | 42     | 6  | BD274280  | BD274280 Identific |
| 4          | 29    | 100.0         | 42     | 6  | BD274281  | BD274281 Identific |
| 5          | 28    | 96.6          | 46     | 6  | BD274241  | BD274241 Identific |
| 6          | 28    | 96.6          | 46     | 6  | BD274242  | BD274242 Identific |
| 7          | 28    | 96.6          | 46     | 6  | BD274243  | BD274243 Identific |
| 8          | 28    | 96.6          | 46     | 6  | BD274258  | BD274258 Identific |
| 9          | 28    | 96.6          | 46     | 6  | BD274259  | BD274259 Identific |
| 10         | 28    | 96.6          | 46     | 6  | BD274260  | BD274260 Identific |
| 11         | 24.8  | 85.5          | 42     | 6  | BD274270  | BD274270 Identific |
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| 13         | 23.8  | 82.1          | 46     | 6  | BD274238  | BD274238 Identific |
| 14         | 23.8  | 82.1          | 46     | 6  | BD274256  | BD274256 Identific |
| 15         | 23.2  | 80.0          | 42     | 6  | BD274275  | BD274275 Identific |
| 16         | 23.2  | 80.0          | 42     | 6  | BD274283  | BD274283 Identific |
| 17         | 22.2  | 76.6          | 46     | 6  | BD274240  | BD274240 Identific |
| 18         | 22.2  | 76.6          | 46     | 6  | BD274249  | BD274249 Identific |
| 19         | 22.2  | 76.6          | 46     | 6  | BD274252  | BD274252 Identific |
| 20         | 22.2  | 76.6          | 46     | 6  | BD274253  | BD274253 Identific |
| 21         | 22.2  | 76.6          | 46     | 6  | BD274257  | BD274257 Identific |
| 22         | 22.2  | 76.6          | 46     | 6  | BD274265  | BD274265 Identific |
| 23         | 22.2  | 76.6          | 46     | 6  | BD274268  | BD274268 Identific |
| 24         | 22.2  | 76.6          | 46     | 6  | BD274269  | BD274269 Identific |
| 25         | 21.2  | 73.1          | 42     | 6  | BD274271  | BD274271 Identific |
| 26         | 21.2  | 73.1          | 42     | 6  | BD274279  | BD274279 Identific |
| 27         | 21.2  | 73.1          | 46     | 6  | BD274247  | BD274247 Identific |
| 28         | 21.2  | 73.1          | 46     | 6  | BD274263  | BD274263 Identific |
| 29         | 20    | 69.0          | 46     | 6  | BD274237  | BD274237 Identific |
| 30         | 20    | 69.0          | 46     | 6  | BD274251  | BD274251 Identific |
| 31         | 20    | 69.0          | 46     | 6  | BD274255  | BD274255 Identific |
| 32         | 20    | 69.0          | 46     | 6  | BD274257  | BD274257 Identific |
| 33         | 19.6  | 67.6          | 42     | 6  | BD274284  | BD274284 Identific |
| 34         | 18.6  | 64.1          | 46     | 6  | BD274246  | BD274246 Identific |
| 35         | 18.6  | 64.1          | 46     | 6  | BD274248  | BD274248 Identific |
| 36         | 18.6  | 64.1          | 46     | 6  | BD274262  | BD274262 Identific |
| 37         | 18.6  | 64.1          | 46     | 6  | BD274264  | BD274264 Identific |
| 38         | 18.4  | 63.4          | 42     | 6  | BD274274  | BD274274 Identific |
| 39         | 18.4  | 63.4          | 42     | 6  | BD274282  | BD274282 Identific |
| 40         | 18.4  | 63.4          | 43     | 8  | ATH553793 | BD274277 Arabidops |
| 41         | 18    | 62.1          | 44     | 6  | BD274277  | BD274277 Identific |
| C 42       | 16.4  | 56.6          | 31     | 6  | AX425989  | AX425989 Sequence  |
| C 43       | 16.4  | 56.6          | 42     | 6  | BD274276  | BD274276 Identific |
| C 44       | 16.2  | 55.9          | 48     | 6  | AX018731  | AX018731 Sequence  |
| C 45       | 16.2  | 55.9          | 79     | 6  | AX914035  | AX914035 Sequence  |
| C 46       | 16.2  | 55.9          | 79     | 6  | BD049568  | BD049568 Sequence  |
| C 47       | 15.4  | 53.1          | 73     | 6  | E02131    | E02131 Pseudoknot  |
| C 48       | 15.2  | 52.4          | 33     | 6  | AR020509  | AR020509 Sequence  |
| C 49       | 15.2  | 52.4          | 47     | 6  | AR289362  | AR289362 Sequence  |
| 50         | 15    | 51.7          | 23     | 6  | E09974    | E09974 Primer for  |
| 51         | 15    | 51.7          | 23     | 6  | E10118    | E10118 PCR primer  |
| 52         | 15    | 51.7          | 30     | 6  | AX793341  | AX793341 Sequence  |
| C 53       | 15    | 51.7          | 33     | 6  | BD094291  | BD094291 A prepara |
| C 54       | 15    | 51.7          | 33     | 6  | BD179370  | BD179370 A novel p |
| C 55       | 15    | 51.7          | 41     | 6  | AX514720  | AX514720 Sequence  |
| C 56       | 15    | 51.7          | 41     | 6  | AX520728  | AX520728 Sequence  |
| C 57       | 15    | 51.7          | 55     | 8  | AJ598912  | AJ598912 Arabidops |
| C 58       | 14.8  | 51.0          | 29     | 6  | AR019319  | AR019319 Sequence  |
| C 59       | 14.8  | 51.0          | 29     | 6  | AR061847  | AR061847 Sequence  |
| C 60       | 14.8  | 51.0          | 29     | 6  | AR147578  | AR147578 Sequence  |
| C 61       | 14.8  | 51.0          | 29     | 6  | BD233978  | BD233978 Multiple  |
| C 62       | 14.8  | 51.0          | 29     | 6  | I34733    | I34733 Sequence 25 |
| C 63       | 14.8  | 51.0          | 29     | 6  | I67987    | I67987 Sequence 25 |
| C 64       | 14.8  | 51.0          | 29     | 6  | AR252838  | AR252838 Sequence  |
| C 65       | 14.8  | 51.0          | 32     | 6  | AR061867  | AR061867 Sequence  |

|       |      |      |    |    |            |                     |       |      |      |    |    |           |                     |
|-------|------|------|----|----|------------|---------------------|-------|------|------|----|----|-----------|---------------------|
| C 66  | 14.8 | 51.0 | 32 | 6  | BD233998   | BD233998 Multiple   | C 139 | 13.8 | 47.6 | 60 | 6  | AX303607  | AX303607 Sequence   |
| C 67  | 14.8 | 51.0 | 32 | 6  | AR252858   | AR252858 Sequence   | 140   | 13.8 | 47.6 | 61 | 6  | AR437950  | AR437950 Sequence   |
| C 68  | 14.8 | 51.0 | 80 | 6  | AS2215     | AS2215 Sequence 5   | 141   | 13.8 | 47.6 | 61 | 6  | AX303592  | AX303592 Sequence   |
| C 69  | 14.6 | 50.3 | 25 | 6  | AR206010   | AR206010 Sequence   | C 142 | 13.8 | 47.6 | 80 | 8  | HSU91041  | U91041 Homo sapiens |
| C 70  | 14.6 | 50.3 | 25 | 6  | AX043294   | AX043294 Sequence   | C 143 | 13.8 | 47.6 | 80 | 8  | AXJ593415 | AXJ593415 Arabidops |
| C 71  | 14.6 | 50.3 | 57 | 8  | AR061021   | AR061021 Sequence   | C 144 | 13.6 | 46.9 | 25 | 6  | AX610026  | AX610026 Sequence   |
| C 72  | 14.6 | 50.3 | 57 | 8  | ARJ591789  | ARJ591789 Arabidops | C 145 | 13.6 | 46.9 | 30 | 9  | HSCD85719 | Z50832 H. sapiens m |
| C 73  | 14.6 | 50.3 | 73 | 6  | AX909836   | AX909836 Sequence   | C 146 | 13.6 | 46.9 | 34 | 9  | AF505532  | AF505532 Homo sapi  |
| C 74  | 14.6 | 50.3 | 73 | 6  | BD045369   | BD045369 Sequence   | C 147 | 13.6 | 46.9 | 39 | 9  | HUMTCDGA  | M28786 Human T-cel  |
| C 75  | 14.4 | 49.7 | 25 | 6  | AX043671   | AX043671 Sequence   | C 148 | 13.6 | 46.9 | 39 | 9  | BD259967  | BD259967 Polynucle  |
| C 76  | 14.4 | 49.7 | 31 | 6  | AX425978   | AX425978 Sequence   | 149   | 13.6 | 46.9 | 41 | 6  | AR179776  | AR179776 Sequence   |
| C 77  | 14.4 | 49.7 | 51 | 6  | AX117185   | AX117185 Sequence   | 150   | 13.6 | 46.9 | 41 | 6  | AX045453  | AX045453 Sequence   |
| C 78  | 14.4 | 49.7 | 59 | 11 | AL772710   | AL772710 Arabidops  | 151   | 13.6 | 46.9 | 41 | 6  | AX045800  | AX045800 Sequence   |
| C 79  | 14.4 | 49.7 | 59 | 11 | AL773039   | AL773039 Arabidops  | C 152 | 13.6 | 46.9 | 43 | 8  | AXJ587991 | AXJ587991 Arabidops |
| C 80  | 14.2 | 49.0 | 25 | 6  | AR434675   | AR434675 Sequence   | C 153 | 13.6 | 46.9 | 47 | 6  | AR4765    | AR4765 Sequence 10  |
| C 81  | 14.2 | 49.0 | 25 | 6  | AR434676   | AR434676 Sequence   | C 154 | 13.6 | 46.9 | 47 | 6  | AR290108  | AR290108 Sequence   |
| C 82  | 14.2 | 49.0 | 25 | 6  | AR434677   | AR434677 Sequence   | C 155 | 13.6 | 46.9 | 47 | 6  | AR300168  | AR300168 Sequence   |
| C 83  | 14.2 | 49.0 | 25 | 6  | AR434678   | AR434678 Sequence   | C 156 | 13.6 | 46.9 | 47 | 6  | BD058055  | BD058055 Method fo  |
| C 84  | 14.2 | 49.0 | 25 | 6  | AR434679   | AR434679 Sequence   | 157   | 13.6 | 46.9 | 52 | 6  | BD270556  | BD270556 Family of  |
| C 85  | 14.2 | 49.0 | 25 | 6  | AR434680   | AR434680 Sequence   | 158   | 13.6 | 46.9 | 52 | 6  | AR208953  | AR208953 Sequence   |
| C 86  | 14.2 | 49.0 | 25 | 6  | AR434681   | AR434681 Sequence   | 159   | 13.6 | 46.9 | 52 | 6  | AR228346  | AR228346 Sequence   |
| C 87  | 14.2 | 49.0 | 30 | 6  | AX792238   | AX792238 Sequence   | 160   | 13.6 | 46.9 | 52 | 6  | AX046943  | AX046943 Sequence   |
| C 88  | 14.2 | 49.0 | 31 | 6  | AX582577   | AX582577 Sequence   | C 161 | 13.6 | 46.9 | 52 | 6  | AX189279  | AX189279 Sequence   |
| C 89  | 14.2 | 49.0 | 42 | 6  | BD274270   | BD274270 Identific  | 162   | 13.6 | 46.9 | 52 | 6  | AX428345  | AX428345 Sequence   |
| C 90  | 14.2 | 49.0 | 42 | 6  | BD274278   | BD274278 Identific  | 163   | 13.6 | 46.9 | 52 | 6  | BD082716  | BD082716 Family of  |
| C 91  | 14.2 | 49.0 | 44 | 6  | AX601758   | AX601758 Sequence   | 164   | 13.6 | 46.9 | 60 | 6  | AX189280  | AX189280 Sequence   |
| C 92  | 14.2 | 49.0 | 47 | 6  | AR288361   | AR288361 Sequence   | 165   | 13.6 | 46.9 | 65 | 6  | AX484957  | AX484957 Sequence   |
| C 93  | 14.2 | 49.0 | 65 | 6  | AX483200   | AX483200 Sequence   | 166   | 13.6 | 46.9 | 69 | 6  | BD161913  | BD161913 Recombina  |
| C 94  | 14.2 | 49.0 | 69 | 6  | AR052905   | AR052905 Sequence   | C 167 | 13.6 | 46.9 | 72 | 11 | AL806183  | AL806183 Arabidops  |
| C 95  | 14.2 | 49.0 | 69 | 6  | AR054269   | AR054269 Sequence   | C 168 | 13.6 | 46.9 | 75 | 11 | AL773214  | AL773214 Arabidops  |
| C 96  | 14.2 | 49.0 | 69 | 6  | AR054471   | AR054471 Sequence   | C 169 | 13.6 | 46.9 | 79 | 6  | AR017735  | AR017735 Sequence   |
| C 97  | 14.2 | 49.0 | 69 | 6  | ATH527686  | ATH527686 Arabidops | C 170 | 13.6 | 46.9 | 79 | 6  | AR094912  | AR094912 Sequence   |
| C 98  | 14.2 | 49.0 | 78 | 8  | ATH527607  | ATH527607 Arabidops | C 171 | 13.6 | 46.9 | 79 | 6  | AR165571  | AR165571 Sequence   |
| C 99  | 14.2 | 49.0 | 78 | 8  | ATH531507  | ATH531507 Arabidops | C 172 | 13.6 | 46.9 | 79 | 6  | AR304769  | AR304769 Sequence   |
| C 100 | 14   | 48.3 | 25 | 6  | AX043055   | AX043055 Sequence   | C 173 | 13.6 | 46.9 | 80 | 8  | ATH526370 | ATH526370 Arabidops |
| C 101 | 14   | 48.3 | 29 | 11 | AL806194   | AL806194 Arabidops  | 174   | 13.6 | 46.9 | 80 | 10 | RNSG18    | G161776 Rat synapto |
| C 102 | 14   | 48.3 | 29 | 11 | AL824524   | AL824524 Arabidops  | 175   | 13.4 | 46.2 | 25 | 6  | AX042556  | AX042556 Sequence   |
| C 103 | 14   | 48.3 | 33 | 11 | AL806370   | AL806370 Arabidops  | 176   | 13.4 | 46.2 | 25 | 6  | AX042557  | AX042557 Sequence   |
| C 104 | 14   | 48.3 | 34 | 11 | AL824530   | AL824530 Arabidops  | 177   | 13.4 | 46.2 | 25 | 6  | AX042570  | AX042570 Sequence   |
| C 105 | 14   | 48.3 | 35 | 11 | AL806140   | AL806140 Arabidops  | 178   | 13.4 | 46.2 | 25 | 6  | AX042575  | AX042575 Sequence   |
| C 106 | 14   | 48.3 | 35 | 11 | AL806354   | AL806354 Arabidops  | 179   | 13.4 | 46.2 | 25 | 6  | AX042625  | AX042625 Sequence   |
| C 107 | 14   | 48.3 | 40 | 11 | AL824626   | AL824626 Arabidops  | 180   | 13.4 | 46.2 | 25 | 6  | AX043147  | AX043147 Sequence   |
| C 108 | 14   | 48.3 | 40 | 11 | AL824634   | AL824634 Arabidops  | 181   | 13.4 | 46.2 | 25 | 6  | AX043173  | AX043173 Sequence   |
| C 109 | 14   | 48.3 | 41 | 6  | AR253879   | AR253879 Sequence   | 182   | 13.4 | 46.2 | 25 | 6  | AX043267  | AX043267 Sequence   |
| C 110 | 14   | 48.3 | 41 | 6  | AX410230   | AX410230 Sequence   | 183   | 13.4 | 46.2 | 25 | 6  | AX043269  | AX043269 Sequence   |
| C 111 | 14   | 48.3 | 41 | 6  | AX316543   | AX316543 Sequence   | 184   | 13.4 | 46.2 | 25 | 6  | AX043288  | AX043288 Sequence   |
| C 112 | 14   | 48.3 | 42 | 11 | AL806268   | AL806268 Arabidops  | 185   | 13.4 | 46.2 | 25 | 6  | AX043479  | AX043479 Sequence   |
| C 113 | 14   | 48.3 | 42 | 11 | AL823473   | AL823473 Arabidops  | 186   | 13.4 | 46.2 | 25 | 6  | AX043558  | AX043558 Sequence   |
| C 114 | 14   | 48.3 | 42 | 11 | AL823519   | AL823519 Arabidops  | 187   | 13.4 | 46.2 | 25 | 6  | AX043602  | AX043602 Sequence   |
| C 115 | 14   | 48.3 | 42 | 11 | AL824624   | AL824624 Arabidops  | 188   | 13.4 | 46.2 | 32 | 6  | AX043611  | AX043611 Sequence   |
| C 116 | 14   | 48.3 | 42 | 11 | AL824629   | AL824629 Arabidops  | 189   | 13.4 | 46.2 | 32 | 6  | AR162666  | AR162666 Sequence   |
| C 117 | 14   | 48.3 | 43 | 11 | AL824507   | AL824507 Arabidops  | 190   | 13.4 | 46.2 | 32 | 6  | AX700013  | AX700013 Sequence   |
| C 118 | 14   | 48.3 | 45 | 11 | AL806303   | AL806303 Arabidops  | 191   | 13.4 | 46.2 | 32 | 6  | BD005937  | BD005937 Human B-C  |
| C 119 | 14   | 48.3 | 45 | 11 | AL823500   | AL823500 Arabidops  | 192   | 13.4 | 46.2 | 32 | 6  | BD185256  | BD185256 Sequence   |
| C 120 | 14   | 48.3 | 48 | 11 | EX323648   | EX323648 Arabidops  | 193   | 13.4 | 46.2 | 34 | 6  | AX282624  | AX282624 Sequence   |
| C 121 | 14   | 48.3 | 75 | 9  | AF313283   | AF313283 Homo sapi  | 194   | 13.4 | 46.2 | 34 | 6  | AX437966  | AX437966 Sequence   |
| C 122 | 13.8 | 47.6 | 27 | 6  | AX249915   | AX249915 Sequence   | C 195 | 13.4 | 46.2 | 40 | 6  | AR437966  | AR437966 Sequence   |
| C 123 | 13.8 | 47.6 | 30 | 6  | AX791584   | AX791584 Sequence   | C 196 | 13.4 | 46.2 | 40 | 6  | AX303610  | AX303610 Sequence   |
| C 124 | 13.8 | 47.6 | 33 | 6  | BD234015   | BD234015 Multiple   | C 197 | 13.4 | 46.2 | 41 | 6  | AX514585  | AX514585 Sequence   |
| C 125 | 13.8 | 47.6 | 33 | 6  | AR252875   | AR252875 Sequence   | C 198 | 13.4 | 46.2 | 41 | 6  | AX520024  | AX520024 Sequence   |
| C 126 | 13.8 | 47.6 | 38 | 9  | HSTCTRDV21 | X69287 H. sapiens m | C 199 | 13.4 | 46.2 | 43 | 6  | AX484576  | AX484576 Sequence   |
| C 127 | 13.8 | 47.6 | 38 | 9  | HSTCTRDV25 | X69287 H. sapiens m | C 200 | 13.4 | 46.2 | 45 | 6  | AX008706  | AX008706 Sequence   |
| C 128 | 13.8 | 47.6 | 40 | 6  | E49126     | E49126 Novel G pro  | C 201 | 13.4 | 46.2 | 45 | 6  | AR032430  | AR032430 Sequence   |
| C 129 | 13.8 | 47.6 | 40 | 6  | E50836     | E50836 Novel G pro  | C 202 | 13.4 | 46.2 | 46 | 6  | AR032433  | AR032433 Sequence   |
| C 130 | 13.8 | 47.6 | 41 | 9  | S80780     | S80780 gamma delta  | C 203 | 13.4 | 46.2 | 46 | 6  | AX032433  | AX032433 Sequence   |
| C 131 | 13.8 | 47.6 | 44 | 6  | AX804136   | AX804136 Sequence   | C 204 | 13.4 | 46.2 | 46 | 6  | I29170    | I29170 Sequence 42  |
| C 132 | 13.8 | 47.6 | 47 | 6  | AR284611   | AR284611 Sequence   | C 205 | 13.4 | 46.2 | 46 | 6  | I29173    | I29173 Sequence 45  |
| C 133 | 13.8 | 47.6 | 50 | 6  | AR437951   | AR437951 Sequence   | C 206 | 13.4 | 46.2 | 46 | 6  | I90844    | I90844 Sequence 42  |
| C 134 | 13.8 | 47.6 | 50 | 6  | AX303593   | AX303593 Sequence   | C 207 | 13.4 | 46.2 | 46 | 6  | I90847    | I90847 Sequence 45  |
| C 135 | 13.8 | 47.6 | 51 | 6  | AX156963   | AX156963 Sequence   | C 208 | 13.4 | 46.2 | 46 | 6  | AR209094  | AR209094 Sequence   |
| C 136 | 13.8 | 47.6 | 57 | 6  | AR437963   | AR437963 Sequence   | C 209 | 13.4 | 46.2 | 46 | 6  | AR209097  | AR209097 Sequence   |
| C 137 | 13.8 | 47.6 | 57 | 6  | AX303606   | AX303606 Sequence   | C 210 | 13.4 | 46.2 | 47 | 6  | AX378367  | AX378367 Sequence   |
| C 138 | 13.8 | 47.6 | 60 | 6  | AR437964   | AR437964 Sequence   | C 211 | 13.4 | 46.2 | 50 | 6  | AR032434  | AR032434 Sequence   |

|       |      |      |    |    |           |                     |       |      |      |    |    |           |                    |
|-------|------|------|----|----|-----------|---------------------|-------|------|------|----|----|-----------|--------------------|
| C 212 | 13.4 | 46.2 | 50 | 6  | I24031    | I24031 Sequence 13  | 285   | 13   | 44.8 | 49 | 6  | I17031    | I17031 Sequence 42 |
| C 213 | 13.4 | 46.2 | 50 | 6  | I29174    | I29174 Sequence 46  | 286   | 13   | 44.8 | 49 | 6  | BD017539  | BD017539 Short-cha |
| C 214 | 13.4 | 46.2 | 50 | 6  | I30848    | I30848 Sequence 46  | C 287 | 13   | 44.8 | 50 | 6  | AX164867  | AX164867 Sequence  |
| C 215 | 13.4 | 46.2 | 50 | 6  | AX209098  | AX209098 Sequence   | C 288 | 13   | 44.8 | 50 | 6  | AX164868  | AX164868 Sequence  |
| C 216 | 13.4 | 46.2 | 51 | 6  | AX199419  | AX199419 Sequence   | C 289 | 13   | 44.8 | 50 | 9  | HUMTGV1   | M18508 Human Val-t |
| C 217 | 13.4 | 46.2 | 51 | 6  | AX199421  | AX199421 Sequence   | C 290 | 13   | 44.8 | 50 | 9  | HUMTGV1   | M18508 Human Val-t |
| C 218 | 13.4 | 46.2 | 51 | 6  | AX198444  | AX198444 Sequence   | C 291 | 13   | 44.8 | 51 | 6  | AX160547  | M18510 Human chime |
| C 219 | 13.4 | 46.2 | 55 | 8  | AJ588102  | AJ588102 Arabidops  | C 292 | 13   | 44.8 | 54 | 6  | I21741    | AX160547 Sequence  |
| C 220 | 13.4 | 46.2 | 60 | 6  | AX743756  | AX743756 Sequence   | C 293 | 13   | 44.8 | 55 | 8  | AJ594929  | I21741 Sequence 7  |
| C 221 | 13.4 | 46.2 | 61 | 6  | AX899355  | AX899355 Sequence   | C 294 | 13   | 44.8 | 56 | 1  | AF087325  | AJ594929 Arabidops |
| C 222 | 13.4 | 46.2 | 63 | 6  | BD034888  | BD034888 Sequence   | C 295 | 13   | 44.8 | 59 | 6  | AX905506  | AF087325 Chlamydia |
| C 223 | 13.4 | 46.2 | 63 | 6  | AF515024  | AF515024 Ginkgo bi  | C 296 | 13   | 44.8 | 59 | 6  | BD041039  | AX905506 Sequence  |
| C 224 | 13.4 | 46.2 | 66 | 8  | AJ600346  | AJ600346 Arabidops  | C 297 | 13   | 44.8 | 59 | 6  | AF205765  | BD041039 Sequence  |
| C 225 | 13.4 | 46.2 | 69 | 8  | HSTRD43A  | Y14702 Human Y143A  | C 298 | 13   | 44.8 | 60 | 10 | AF205765  | AF205765 Mus muscu |
| C 226 | 13.4 | 46.2 | 70 | 5  | CUPC0C22  | Y15104 C-japonica   | C 299 | 13   | 44.8 | 60 | 12 | SYNANVAA  | ME0029 Avian neovi |
| C 227 | 13.4 | 46.2 | 72 | 8  | ATH528801 | AJ528801 Arabidops  | C 300 | 13   | 44.8 | 63 | 9  | AX152473  | AX152473 Homo sapi |
| C 228 | 13.4 | 46.2 | 72 | 8  | ATH528801 | AJ528801 Arabidops  | C 301 | 13   | 44.8 | 64 | 6  | AX798145  | AX798145 Sequence  |
| C 229 | 13.4 | 46.2 | 73 | 8  | ATH531238 | AJ531238 Arabidops  | C 302 | 13   | 44.8 | 64 | 6  | AX798953  | AX798953 Sequence  |
| C 230 | 13.4 | 46.2 | 78 | 8  | ATH531238 | AJ531238 Arabidops  | C 303 | 13   | 44.8 | 65 | 6  | AX483133  | AX483133 Sequence  |
| C 231 | 13.2 | 45.5 | 25 | 6  | AR434674  | AR434674 Sequence   | C 304 | 13   | 44.8 | 65 | 6  | AX486145  | AX486145 Sequence  |
| C 232 | 13.2 | 45.5 | 25 | 6  | AR434682  | AR434682 Sequence   | C 305 | 13   | 44.8 | 66 | 8  | AF515023  | AX486145 Sequence  |
| C 233 | 13.2 | 45.5 | 27 | 6  | I81984    | I81984 Sequence 23  | C 306 | 13   | 44.8 | 66 | 10 | AX177480  | AF515023 Ginkgo bi |
| C 234 | 13.2 | 45.5 | 28 | 6  | BD083583  | BD083583 A porin g  | C 307 | 13   | 44.8 | 68 | 6  | AR242687  | AX177480 Mus muscu |
| C 235 | 13.2 | 45.5 | 31 | 6  | AX425725  | AX425725 Sequence   | C 308 | 13   | 44.8 | 70 | 6  | AR054926  | AR242687 Sequence  |
| C 236 | 13.2 | 45.5 | 32 | 6  | AX371800  | AX371800 Sequence   | C 309 | 13   | 44.8 | 70 | 6  | AR066191  | AR054926 Sequence  |
| C 237 | 13.2 | 45.5 | 37 | 6  | AX465693  | AX465693 Sequence   | C 310 | 13   | 44.8 | 72 | 8  | ATH528433 | AR066191 Sequence  |
| C 238 | 13.2 | 45.5 | 38 | 6  | AR046687  | AR046687 Sequence   | C 311 | 13   | 44.8 | 72 | 8  | AX903224  | AJ528433 Arabidops |
| C 239 | 13.2 | 45.5 | 38 | 6  | AR057865  | AR057865 Sequence   | C 312 | 13   | 44.8 | 73 | 6  | BD038757  | AX903224 Sequence  |
| C 240 | 13.2 | 45.5 | 38 | 6  | AR115623  | AR115623 Sequence   | C 313 | 13   | 44.8 | 73 | 6  | S60869    | BD038757 Sequence  |
| C 241 | 13.2 | 45.5 | 38 | 6  | I53739    | I53739 Sequence 14  | C 314 | 13   | 44.8 | 73 | 9  | S60869    | S60869 TCRB (t1;7  |
| C 242 | 13.2 | 45.5 | 38 | 6  | AX634924  | AX634924 Sequence   | C 315 | 13   | 44.8 | 75 | 6  | E02130    | E02130 Pseudoknot  |
| C 243 | 13.2 | 45.5 | 40 | 9  | AF505564  | AF505564 Homo sapi  | C 316 | 13   | 44.8 | 76 | 8  | AJ598926  | AJ598926 Arabidops |
| C 244 | 13.2 | 45.5 | 41 | 6  | AX516773  | AX516773 Sequence   | C 317 | 13   | 44.8 | 77 | 6  | BD035233  | AX598926 Sequence  |
| C 245 | 13.2 | 45.5 | 45 | 6  | I04390    | I04390 Sequence 25  | C 318 | 13   | 44.8 | 77 | 6  | AR007410  | BD035233 Sequence  |
| C 246 | 13.2 | 45.5 | 47 | 6  | AR290116  | AR290116 Sequence   | C 319 | 12.8 | 44.1 | 78 | 6  | BD177994  | AR007410 Sequence  |
| C 247 | 13.2 | 45.5 | 51 | 6  | E22334    | E22334 DNA encodin  | C 320 | 12.8 | 44.1 | 16 | 6  | AX255822  | BD177994 Acylated  |
| C 248 | 13.2 | 45.5 | 51 | 6  | E22334    | E22334 DNA encodin  | C 321 | 12.8 | 44.1 | 16 | 6  | AX255822  | AX255822 Sequence  |
| C 249 | 13.2 | 45.5 | 51 | 6  | AX204336  | AX204336 Sequence   | C 322 | 12.8 | 44.1 | 18 | 6  | AR293731  | AX255822 Sequence  |
| C 250 | 13.2 | 45.5 | 57 | 9  | HSU91098  | U91098 Homo sapien  | C 323 | 12.8 | 44.1 | 20 | 6  | AR092414  | AR293731 Sequence  |
| C 251 | 13.2 | 45.5 | 59 | 6  | E22349    | E22349 DNA encodin  | C 324 | 12.8 | 44.1 | 20 | 6  | AX353716  | AR092414 Sequence  |
| C 252 | 13.2 | 45.5 | 62 | 9  | AB010672  | AB010672 Homo sapi  | C 325 | 12.8 | 44.1 | 20 | 6  | AX082340  | AX353716 Sequence  |
| C 253 | 13.2 | 45.5 | 64 | 6  | AR009650  | AR009650 Sequence   | C 326 | 12.8 | 44.1 | 20 | 6  | AX613386  | AX082340 Sequence  |
| C 254 | 13.2 | 45.5 | 66 | 6  | HS081414  | HS081414 Human GDH1 | C 327 | 12.8 | 44.1 | 22 | 6  | AX613388  | AX613386 Sequence  |
| C 255 | 13.2 | 45.5 | 66 | 6  | E16843    | E16843 PCR primer   | C 328 | 12.8 | 44.1 | 23 | 6  | BD205443  | AX613388 Sequence  |
| C 256 | 13.2 | 45.5 | 66 | 6  | AR356613  | AR356613 Sequence   | C 329 | 12.8 | 44.1 | 23 | 6  | BD205443  | BD205443 Recombina |
| C 257 | 13.2 | 45.5 | 69 | 6  | BD246652  | BD246652 Developme  | C 330 | 12.8 | 44.1 | 24 | 6  | AX493027  | BD205443 Sequence  |
| C 258 | 13.2 | 45.5 | 69 | 6  | AR341695  | AR341695 Sequence   | C 331 | 12.8 | 44.1 | 24 | 6  | MMBR242   | AX493027 Sequence  |
| C 259 | 13.2 | 45.5 | 17 | 6  | AX757248  | AX757248 Sequence   | C 332 | 12.8 | 44.1 | 24 | 10 | MMBR242   | BD057100 Polymetas |
| C 260 | 13   | 44.8 | 24 | 6  | AX801575  | AX801575 Sequence   | C 333 | 12.8 | 44.1 | 25 | 6  | AX043436  | AX4824 M.musculus  |
| C 261 | 13   | 44.8 | 24 | 6  | AX801575  | AX801575 Sequence   | C 334 | 12.8 | 44.1 | 25 | 6  | BD255986  | AX043436 Sequence  |
| C 262 | 13   | 44.8 | 25 | 6  | AX042898  | AX042898 Sequence   | C 335 | 12.8 | 44.1 | 30 | 6  | AS6993    | BD255986 Regulatio |
| C 263 | 13   | 44.8 | 25 | 6  | AX042924  | AX042924 Sequence   | C 336 | 12.8 | 44.1 | 30 | 6  | AS6993    | AS6993 Sequence 51 |
| C 264 | 13   | 44.8 | 25 | 6  | AX043101  | AX043101 Sequence   | C 337 | 12.8 | 44.1 | 31 | 6  | AX223316  | AS6993 Sequence 51 |
| C 265 | 13   | 44.8 | 25 | 6  | AX043335  | AX043335 Sequence   | C 338 | 12.8 | 44.1 | 31 | 6  | AR016863  | AX223316 Sequence  |
| C 266 | 13   | 44.8 | 25 | 6  | AR039472  | AR039472 Sequence   | C 339 | 12.8 | 44.1 | 33 | 6  | AR020889  | AX223401 Sequence  |
| C 267 | 13   | 44.8 | 27 | 6  | AR040432  | AR040432 Sequence   | C 340 | 12.8 | 44.1 | 33 | 6  | AR020889  | AX223401 Sequence  |
| C 268 | 13   | 44.8 | 31 | 6  | AX220837  | AX220837 Sequence   | C 341 | 12.8 | 44.1 | 33 | 6  | AR027212  | AR020889 Sequence  |
| C 269 | 13   | 44.8 | 31 | 6  | BD002854  | BD002854 Gene comp  | C 342 | 12.8 | 44.1 | 33 | 6  | AR064641  | AR027212 Sequence  |
| C 270 | 13   | 44.8 | 34 | 6  | AR089711  | AR089711 Sequence   | C 343 | 12.8 | 44.1 | 33 | 6  | AR064641  | AR064641 Sequence  |
| C 271 | 13   | 44.8 | 36 | 6  | AX052576  | AX052576 Sequence   | C 344 | 12.8 | 44.1 | 33 | 6  | AR083737  | AR064641 Sequence  |
| C 272 | 13   | 44.8 | 38 | 6  | AX05024   | AX05024 Oligonucleo | C 345 | 12.8 | 44.1 | 33 | 6  | I38518    | AR083737 Sequence  |
| C 273 | 13   | 44.8 | 38 | 6  | AX08145   | AX08145 Oligonucleo | C 346 | 12.8 | 44.1 | 33 | 6  | I56993    | I38518 Sequence 96 |
| C 274 | 13   | 44.8 | 38 | 6  | AX13246   | AX13246 Oligonucleo | C 347 | 12.8 | 44.1 | 33 | 6  | I56993    | I56993 Sequence 96 |
| C 275 | 13   | 44.8 | 38 | 6  | I33196    | I33196 Sequence 19  | C 348 | 12.8 | 44.1 | 33 | 6  | I75186    | I56993 Sequence 96 |
| C 276 | 13   | 44.8 | 38 | 6  | I40175    | I40175 Sequence 19  | C 349 | 12.8 | 44.1 | 33 | 6  | AR270966  | I75186 Sequence 96 |
| C 277 | 13   | 44.8 | 38 | 6  | I40407    | I40407 Sequence 19  | C 350 | 12.8 | 44.1 | 35 | 6  | AR270966  | AR270966 Sequence  |
| C 278 | 13   | 44.8 | 38 | 6  | AX219881  | AX219881 Sequence   | C 351 | 12.8 | 44.1 | 35 | 11 | C75880    | AR270966 Sequence  |
| C 279 | 13   | 44.8 | 40 | 8  | BOL293429 | AJ293429 Brassica   | C 352 | 12.8 | 44.1 | 36 | 6  | I39294    | C75880 Homo sapien |
| C 280 | 13   | 44.8 | 41 | 6  | AX515635  | AX515635 Sequence   | C 353 | 12.8 | 44.1 | 36 | 6  | AX635571  | I39294 Sequence 33 |
| C 281 | 13   | 44.8 | 41 | 6  | AX519230  | AX519230 Sequence   | C 354 | 12.8 | 44.1 | 39 | 6  | AX574443  | AX635571 Sequence  |
| C 282 | 13   | 44.8 | 45 | 10 | RATMLV5   | M23125 Rat provira  | C 355 | 12.8 | 44.1 | 40 | 6  | AR053634  | AX574443 Sequence  |
| C 283 | 13   | 44.8 | 47 | 6  | AR291107  | AR291107 Sequence   | C 356 | 12.8 | 44.1 | 40 | 6  | AX258569  | AR053634 Sequence  |
| C 284 | 13   | 44.8 | 48 | 9  | S81456    | S81456 T cell anti  | C 357 | 12.8 | 44.1 | 40 | 6  | AX496010  | AX258569 Sequence  |

|       |      |      |    |    |            |                    |       |      |      |    |    |           |                     |
|-------|------|------|----|----|------------|--------------------|-------|------|------|----|----|-----------|---------------------|
| 358   | 12.8 | 44.1 | 41 | 6  | AX516373   | AX516373 Sequence  | 431   | 12.6 | 43.4 | 36 | 6  | AR112727  | AR112727 Sequence   |
| 359   | 12.8 | 44.1 | 41 | 6  | AX518935   | AX518935 Sequence  | C 432 | 12.6 | 43.4 | 36 | 6  | AR176463  | AR176463 Sequence   |
| 360   | 12.8 | 44.1 | 41 | 6  | AX518936   | AX518936 Sequence  | C 433 | 12.6 | 43.4 | 36 | 6  | AR176468  | AR176468 Sequence   |
| C 361 | 12.8 | 44.1 | 41 | 6  | AX519782   | AX519782 Sequence  | C 434 | 12.6 | 43.4 | 36 | 6  | AX468257  | AX468257 Sequence   |
| 362   | 12.8 | 44.1 | 41 | 6  | AX520403   | AX520403 Sequence  | C 435 | 12.6 | 43.4 | 41 | 6  | AX516946  | AX516946 Sequence   |
| C 363 | 12.8 | 44.1 | 43 | 6  | AR169518   | AR169518 Sequence  | C 436 | 12.6 | 43.4 | 41 | 6  | AX518206  | AX518206 Sequence   |
| C 364 | 12.8 | 44.1 | 43 | 6  | AR169518   | AR169518 Sequence  | C 437 | 12.6 | 43.4 | 41 | 6  | AX519457  | AX519457 Sequence   |
| 365   | 12.8 | 44.1 | 45 | 9  | S80711     | S80711 gamma delta | C 438 | 12.6 | 43.4 | 42 | 6  | AR139460  | AR139460 Sequence   |
| 366   | 12.8 | 44.1 | 47 | 6  | AR290646   | AR290646 Sequence  | C 439 | 12.6 | 43.4 | 42 | 6  | BD274275  | BD274275 Identific  |
| 367   | 12.8 | 44.1 | 50 | 6  | AX23415    | AX23415 Sequence   | C 440 | 12.6 | 43.4 | 42 | 6  | BD274283  | BD274283 Identific  |
| 368   | 12.8 | 44.1 | 50 | 9  | HUMSAU3A07 | D49591 Homo sapien | C 441 | 12.6 | 43.4 | 42 | 6  | E22565    | E22565 Process for  |
| 369   | 12.8 | 44.1 | 50 | 9  | HUMSAU3A10 | D49594 Homo sapien | C 442 | 12.6 | 43.4 | 42 | 6  | E22566    | E22566 Process for  |
| 370   | 12.8 | 44.1 | 54 | 6  | HUMSAU3A66 | D49650 Homo sapien | C 443 | 12.6 | 43.4 | 42 | 6  | E25724    | E25724 Method for   |
| 371   | 12.8 | 44.1 | 54 | 6  | AR098551   | AR098551 Sequence  | C 444 | 12.6 | 43.4 | 42 | 6  | AR364415  | AR364415 Sequence   |
| 372   | 12.8 | 44.1 | 54 | 6  | AR108893   | AR108893 Sequence  | C 445 | 12.6 | 43.4 | 42 | 10 | S77066    | S77066 T-cell rece  |
| 373   | 12.8 | 44.1 | 54 | 6  | AR268150   | AR268150 Sequence  | C 446 | 12.6 | 43.4 | 43 | 6  | AR004641  | AR004641 Sequence   |
| 374   | 12.8 | 44.1 | 54 | 6  | AX009660   | AX009660 Sequence  | C 447 | 12.6 | 43.4 | 43 | 6  | AR034553  | AR034553 Sequence   |
| C 375 | 12.8 | 44.1 | 54 | 6  | AX010922   | AX010922 Sequence  | C 448 | 12.6 | 43.4 | 43 | 6  | 189243    | 189243 Sequence 4   |
| 376   | 12.8 | 44.1 | 57 | 8  | AJ587751   | AJ587751 Arabidops | C 449 | 12.6 | 43.4 | 43 | 8  | AJ599099  | AJ599099 Arabidops  |
| 377   | 12.8 | 44.1 | 57 | 7  | SP17F1D    | M14288 Bacterioph  | C 450 | 12.6 | 43.4 | 44 | 6  | AX601763  | AX601763 Sequence   |
| 378   | 12.8 | 44.1 | 60 | 9  | HUMSAU3A41 | D49625 Homo sapien | C 451 | 12.6 | 43.4 | 45 | 6  | A76523    | A76523 Sequence 4   |
| 379   | 12.8 | 44.1 | 60 | 9  | HUMSAU3A42 | D49626 Homo sapien | C 452 | 12.6 | 43.4 | 45 | 6  | AR032518  | AR032518 Sequence   |
| 380   | 12.8 | 44.1 | 60 | 9  | HUMSAU3A44 | D49628 Homo sapien | C 453 | 12.6 | 43.4 | 45 | 6  | AR032730  | AR032730 Sequence   |
| 381   | 12.8 | 44.1 | 61 | 6  | I65507     | I65507 Sequence 3  | C 454 | 12.6 | 43.4 | 45 | 6  | 129358    | 129358 Sequence 13  |
| C 382 | 12.8 | 44.1 | 63 | 9  | HUMUT68A01 | L22543 Human chrom | C 455 | 12.6 | 43.4 | 45 | 6  | 129470    | 129470 Sequence 34  |
| 383   | 12.8 | 44.1 | 65 | 6  | AX399385   | AX399385 Sequence  | C 456 | 12.6 | 43.4 | 45 | 6  | 190932    | 190932 Sequence 13  |
| C 384 | 12.8 | 44.1 | 65 | 6  | AX483725   | AX483725 Sequence  | C 457 | 12.6 | 43.4 | 45 | 6  | 191144    | 191144 Sequence 34  |
| 385   | 12.8 | 44.1 | 65 | 6  | AX483961   | AX483961 Sequence  | C 458 | 12.6 | 43.4 | 45 | 6  | AR209182  | AR209182 Sequence   |
| C 386 | 12.8 | 44.1 | 66 | 7  | PP1C2611I  | M13326 Bacterioph  | C 459 | 12.6 | 43.4 | 45 | 6  | AR209394  | AR209394 Sequence   |
| 387   | 12.8 | 44.1 | 66 | 7  | PP1CIN22L  | M13314 Bacterioph  | C 460 | 12.6 | 43.4 | 46 | 6  | BD274250  | BD274250 Identific  |
| 388   | 12.8 | 44.1 | 66 | 7  | PP1CN2611I | M13325 Bacterioph  | C 461 | 12.6 | 43.4 | 46 | 8  | ATH522083 | ATH522083 Arabidops |
| 389   | 12.8 | 44.1 | 69 | 6  | AR171551   | AR171551 Sequence  | C 462 | 12.6 | 43.4 | 47 | 6  | AX770059  | AX770059 Sequence   |
| C 390 | 12.8 | 44.1 | 69 | 6  | AX900803   | AX900803 Sequence  | C 463 | 12.6 | 43.4 | 48 | 6  | AX003185  | AX003185 Sequence   |
| 391   | 12.8 | 44.1 | 69 | 6  | AX904939   | AX904939 Sequence  | C 464 | 12.6 | 43.4 | 48 | 6  | BD195003  | BD195003 Equine in  |
| 392   | 12.8 | 44.1 | 69 | 6  | BD005571   | BD005571 Compositi | C 465 | 12.6 | 43.4 | 49 | 6  | AR403952  | AR403952 Sequence   |
| C 393 | 12.8 | 44.1 | 69 | 6  | BD036336   | BD036336 Sequence  | C 466 | 12.6 | 43.4 | 49 | 6  | AR403953  | AR403953 Sequence   |
| 394   | 12.8 | 44.1 | 69 | 6  | BD040472   | BD040472 Sequence  | C 467 | 12.6 | 43.4 | 49 | 6  | AX306319  | AX306319 Sequence   |
| 395   | 12.8 | 44.1 | 70 | 8  | YSCMTOR12A | M34152 S.cerevisia | C 468 | 12.6 | 43.4 | 50 | 6  | AR032731  | AR032731 Sequence   |
| 396   | 12.8 | 44.1 | 71 | 6  | AR089299   | AR089299 Sequence  | C 469 | 12.6 | 43.4 | 50 | 6  | E43956    | E43956 Method of n  |
| 397   | 12.8 | 44.1 | 71 | 6  | 122311     | 122311 Sequence 39 | C 470 | 12.6 | 43.4 | 50 | 6  | 129471    | 129471 Sequence 34  |
| 398   | 12.8 | 44.1 | 71 | 9  | S6616781   | S66167 sterol regu | C 471 | 12.6 | 43.4 | 50 | 6  | 191145    | 191145 Sequence 34  |
| 399   | 12.8 | 44.1 | 72 | 12 | SYNMYCA35S | M19736 Cauliflower | C 472 | 12.6 | 43.4 | 50 | 6  | AR209395  | AR209395 Sequence   |
| C 400 | 12.8 | 44.1 | 73 | 8  | ATH551623  | AJ551623 Arabidops | C 473 | 12.6 | 43.4 | 50 | 6  | AX097512  | AX097512 Sequence   |
| C 401 | 12.8 | 44.1 | 76 | 8  | AF276642   | AF276642 Silene pa | C 474 | 12.6 | 43.4 | 50 | 6  | AX161234  | AX161234 Sequence   |
| 402   | 12.8 | 44.1 | 79 | 6  | AX903724   | AX903724 Sequence  | C 475 | 12.6 | 43.4 | 50 | 6  | AR193638  | AR193638 Sequence   |
| C 403 | 12.8 | 44.1 | 79 | 6  | BD039257   | BD039257 Sequence  | C 476 | 12.6 | 43.4 | 51 | 6  | AR352362  | AR352362 Sequence   |
| C 404 | 12.6 | 43.4 | 19 | 6  | I40121     | I40121 Sequence 3  | C 477 | 12.6 | 43.4 | 51 | 6  | AX199226  | AX199226 Sequence   |
| C 405 | 12.6 | 43.4 | 19 | 6  | AX353501   | AX353501 Sequence  | C 478 | 12.6 | 43.4 | 52 | 6  | I05057    | I05057 Sequence 3   |
| C 406 | 12.6 | 43.4 | 20 | 6  | AX056605   | AX056605 Sequence  | C 479 | 12.6 | 43.4 | 52 | 6  | AX711215  | AX711215 Sequence   |
| C 407 | 12.6 | 43.4 | 21 | 6  | AX097209   | AX097209 Sequence  | C 480 | 12.6 | 43.4 | 53 | 6  | BD271051  | BD271051 Method an  |
| C 408 | 12.6 | 43.4 | 23 | 6  | E49313     | E49313 Infectious  | C 481 | 12.6 | 43.4 | 54 | 6  | AR258457  | AR258457 Sequence   |
| C 409 | 12.6 | 43.4 | 23 | 6  | AR269171   | AR269171 Sequence  | C 482 | 12.6 | 43.4 | 54 | 6  | AR258457  | AR258457 Sequence   |
| C 410 | 12.6 | 43.4 | 23 | 6  | BD015896   | BD015896 Infectiou | C 483 | 12.6 | 43.4 | 56 | 8  | NTA538405 | AJ538405 Nicotiana  |
| C 411 | 12.6 | 43.4 | 23 | 6  | BD016264   | BD016264 Infectiou | C 484 | 12.6 | 43.4 | 59 | 6  | AX917271  | AX917271 Sequence   |
| C 412 | 12.6 | 43.4 | 26 | 6  | AR146828   | AR146828 Sequence  | C 485 | 12.6 | 43.4 | 59 | 6  | BD052804  | BD052804 Sequence   |
| C 413 | 12.6 | 43.4 | 26 | 6  | E22835     | E22835 Promoter se | C 486 | 12.6 | 43.4 | 60 | 6  | A38678    | A38678 Sequence 9   |
| C 414 | 12.6 | 43.4 | 26 | 8  | ATH529956  | AJ529956 Arabidops | C 487 | 12.6 | 43.4 | 61 | 9  | AB010652  | AB010652 Homo sapi  |
| C 415 | 12.6 | 43.4 | 27 | 6  | AX454931   | AX454931 Sequence  | C 488 | 12.6 | 43.4 | 62 | 6  | AR086810  | AR086810 Sequence   |
| C 416 | 12.6 | 43.4 | 29 | 6  | AX024178   | AX024178 Sequence  | C 489 | 12.6 | 43.4 | 62 | 6  | AR181439  | AR181439 Sequence   |
| C 417 | 12.6 | 43.4 | 30 | 6  | A27256     | A27256 Synthetic G | C 490 | 12.6 | 43.4 | 62 | 6  | AX306321  | AX306321 Sequence   |
| C 418 | 12.6 | 43.4 | 30 | 6  | A56895     | A56895 Sequence 8  | C 491 | 12.6 | 43.4 | 64 | 11 | HSU64685  | U64665 Human chrom  |
| C 419 | 12.6 | 43.4 | 30 | 6  | AR242736   | AR242736 Sequence  | C 492 | 12.6 | 43.4 | 65 | 6  | AX306322  | AX306322 Sequence   |
| C 420 | 12.6 | 43.4 | 31 | 6  | AX249086   | AX249086 Sequence  | C 493 | 12.6 | 43.4 | 65 | 6  | AX306323  | AX306323 Sequence   |
| C 421 | 12.6 | 43.4 | 31 | 6  | AX274078   | AX274078 Sequence  | C 494 | 12.6 | 43.4 | 65 | 6  | AX485715  | AX485715 Sequence   |
| C 422 | 12.6 | 43.4 | 31 | 6  | AX425595   | AX425595 Sequence  | C 495 | 12.6 | 43.4 | 66 | 8  | AB028030  | AB028030 Candida 8  |
| C 423 | 12.6 | 43.4 | 31 | 6  | AX426095   | AX426095 Sequence  | C 496 | 12.6 | 43.4 | 69 | 6  | AR055087  | AR055087 Sequence   |
| C 424 | 12.6 | 43.4 | 35 | 6  | AR004640   | AR004640 Sequence  | C 497 | 12.6 | 43.4 | 69 | 6  | AR156336  | AR156336 Sequence   |
| C 425 | 12.6 | 43.4 | 35 | 6  | AR034552   | AR034552 Sequence  | C 498 | 12.6 | 43.4 | 70 | 6  | AX306320  | AX306320 Sequence   |
| C 426 | 12.6 | 43.4 | 35 | 6  | I89242     | I89242 Sequence 3  | C 499 | 12.6 | 43.4 | 72 | 6  | AR086808  | AR086808 Sequence   |
| C 427 | 12.6 | 43.4 | 35 | 6  | AR364414   | AR364414 Sequence  | C 500 | 12.6 | 43.4 | 74 | 6  | AX701724  | AX701724 Sequence   |
| C 428 | 12.6 | 43.4 | 35 | 11 | C75883     | C75883 Homo sapien | C 501 | 12.6 | 43.4 | 76 | 6  | AX906465  | AX906465 Sequence   |
| C 429 | 12.6 | 43.4 | 36 | 6  | AR034089   | AR034089 Sequence  | C 502 | 12.6 | 43.4 | 76 | 6  | BD041998  | BD041998 Sequence   |
| 430   | 12.6 | 43.4 | 36 | 6  | AR071311   | AR071311 Sequence  | C 503 | 12.6 | 43.4 | 77 | 6  | AR009153  | AR009153 Sequence   |



|       |      |      |    |    |           |                     |       |      |      |    |    |            |                      |
|-------|------|------|----|----|-----------|---------------------|-------|------|------|----|----|------------|----------------------|
| C 504 | 12.6 | 43.4 | 77 | 6  | I32419    | I32419 Sequence 1   | C 577 | 12.4 | 42.8 | 71 | 9  | HUMTCGXF   | M12957 Human T-cell  |
| C 505 | 12.6 | 43.4 | 77 | 8  | SOBCPRMF  | K00313 S.obliquus   | 578   | 12.4 | 42.8 | 72 | 8  | ATH528711  | AJ528711 Arabidops   |
| C 506 | 12.6 | 43.4 | 78 | 6  | AR129100  | AR129100 Sequence   | 579   | 12.4 | 42.8 | 73 | 6  | AX344130   | AX344130 Sequence    |
| C 507 | 12.6 | 43.4 | 78 | 6  | BD243451  | BD243451 Nucleic a  | 580   | 12.4 | 42.8 | 80 | 11 | HUMSWX1361 | L41964 Human chrom   |
| C 508 | 12.6 | 43.4 | 79 | 9  | S60076    | S60076 T-cell anti  | 581   | 12.2 | 42.1 | 17 | 6  | AR047002   | AR047002 Sequence 17 |
| C 509 | 12.6 | 43.4 | 79 | 8  | AJ593501  | AJ593501 Arabidops  | 582   | 12.2 | 42.1 | 17 | 6  | IS4054     | IS4054 Sequence 17   |
| C 510 | 12.6 | 43.4 | 79 | 8  | AX165746  | AX165746 Alnus glu  | C 583 | 12.2 | 42.1 | 17 | 6  | AR433858   | AR433858 Sequence    |
| C 511 | 12.4 | 42.8 | 17 | 6  | AX671567  | AX671567 Sequence   | C 584 | 12.2 | 42.1 | 17 | 6  | AR433859   | AR433859 Sequence    |
| C 512 | 12.4 | 42.8 | 17 | 6  | AX761359  | AX761359 Sequence   | C 585 | 12.2 | 42.1 | 17 | 6  | AR433860   | AR433860 Sequence    |
| C 513 | 12.4 | 42.8 | 22 | 6  | AR403671  | AR403671 Sequence   | C 586 | 12.2 | 42.1 | 17 | 6  | AX578839   | AX578839 Sequence    |
| C 514 | 12.4 | 42.8 | 22 | 6  | AX111296  | AX111296 Sequence   | C 587 | 12.2 | 42.1 | 20 | 6  | AR315845   | AR315845 Sequence    |
| C 515 | 12.4 | 42.8 | 22 | 6  | BD106724  | BD106724 Plasti d p | C 588 | 12.2 | 42.1 | 20 | 6  | AR337676   | AR337676 Sequence    |
| C 516 | 12.4 | 42.8 | 25 | 6  | AX042970  | AX042970 Sequence   | C 589 | 12.2 | 42.1 | 20 | 6  | BD131949   | BD131949 Oligonuci   |
| C 517 | 12.4 | 42.8 | 25 | 6  | AX609702  | AX609702 Sequence   | C 590 | 12.2 | 42.1 | 21 | 6  | AX705969   | AX705969 Sequence    |
| C 518 | 12.4 | 42.8 | 25 | 6  | BD061691  | BD061691 Antigenic  | C 591 | 12.2 | 42.1 | 21 | 6  | BD090087   | BD090087 A method    |
| C 519 | 12.4 | 42.8 | 28 | 6  | AR218348  | AR218348 Sequence   | C 592 | 12.2 | 42.1 | 21 | 12 | AB068906   | AB068906 Synthetic   |
| C 520 | 12.4 | 42.8 | 30 | 6  | AR023798  | AR023798 Sequence   | C 593 | 12.2 | 42.1 | 22 | 6  | AR374301   | AR374301 Sequence    |
| C 521 | 12.4 | 42.8 | 30 | 6  | AR110029  | AR110029 Sequence   | 594   | 12.2 | 42.1 | 24 | 6  | AX493334   | AX493334 Sequence    |
| C 522 | 12.4 | 42.8 | 30 | 6  | BD008893  | BD008893 High leve  | C 595 | 12.2 | 42.1 | 25 | 6  | AR381729   | AR381729 Sequence    |
| C 523 | 12.4 | 42.8 | 30 | 6  | BD144237  | BD144237 Monoclonal | C 596 | 12.2 | 42.1 | 25 | 6  | AR434673   | AR434673 Sequence    |
| C 524 | 12.4 | 42.8 | 31 | 6  | AX221027  | AX221027 Sequence   | C 597 | 12.2 | 42.1 | 25 | 6  | AR434683   | AR434683 Sequence    |
| C 525 | 12.4 | 42.8 | 32 | 6  | E16472    | E16472 PCR primer.  | C 598 | 12.2 | 42.1 | 25 | 6  | AX006972   | AX006972 Sequence    |
| C 526 | 12.4 | 42.8 | 32 | 6  | E27643    | E27643 Recombinant  | 599   | 12.2 | 42.1 | 25 | 6  | AX006973   | AX006973 Sequence    |
| C 527 | 12.4 | 42.8 | 33 | 6  | AR219845  | AR219845 Sequence   | 600   | 12.2 | 42.1 | 25 | 6  | AX043040   | AX043040 Sequence    |
| C 528 | 12.4 | 42.8 | 34 | 6  | AR381466  | AR381466 Sequence   | 601   | 12.2 | 42.1 | 25 | 6  | AX043439   | AX043439 Sequence    |
| C 529 | 12.4 | 42.8 | 34 | 6  | AR381469  | AR381469 Sequence   | 602   | 12.2 | 42.1 | 25 | 6  | AX117932   | AX117932 Sequence    |
| C 530 | 12.4 | 42.8 | 37 | 6  | AR003420  | AR003420 Sequence   | C 603 | 12.2 | 42.1 | 25 | 6  | BD217278   | BD217278 Specific    |
| C 531 | 12.4 | 42.8 | 37 | 6  | I21209    | I21209 Sequence 55  | 604   | 12.2 | 42.1 | 25 | 6  | BD217279   | BD217279 Specific    |
| C 532 | 12.4 | 42.8 | 37 | 6  | I74476    | I74476 Sequence 55  | C 605 | 12.2 | 42.1 | 25 | 6  | AX705971   | AX705971 Sequence    |
| C 533 | 12.4 | 42.8 | 38 | 6  | AR331044  | AR331044 Sequence   | C 606 | 12.2 | 42.1 | 29 | 6  | AR018900   | AR018900 Sequence    |
| C 534 | 12.4 | 42.8 | 38 | 6  | AX222612  | AX222612 Sequence   | C 607 | 12.2 | 42.1 | 29 | 6  | AR066528   | AR066528 Sequence    |
| C 535 | 12.4 | 42.8 | 40 | 6  | AX138451  | AX138451 Sequence   | C 608 | 12.2 | 42.1 | 29 | 6  | AR112066   | AR112066 Sequence    |
| C 536 | 12.4 | 42.8 | 40 | 6  | BD015619  | BD015619 Slidable   | C 609 | 12.2 | 42.1 | 29 | 6  | I72245     | I72245 Sequence 22   |
| C 537 | 12.4 | 42.8 | 41 | 6  | AX519781  | AX519781 Sequence   | C 610 | 12.2 | 42.1 | 29 | 6  | I76812     | I76812 Sequence 22   |
| C 538 | 12.4 | 42.8 | 42 | 6  | A70930    | A70930 Sequence 10  | 611   | 12.2 | 42.1 | 29 | 6  | AR254606   | AR254606 Sequence    |
| C 539 | 12.4 | 42.8 | 42 | 6  | BD003415  | BD003415 Soluble p  | 612   | 12.2 | 42.1 | 30 | 6  | A67214     | A67214 Sequence 3    |
| C 540 | 12.4 | 42.8 | 44 | 6  | AR003419  | AR003419 Sequence   | 613   | 12.2 | 42.1 | 30 | 6  | AR076866   | AR076866 Sequence    |
| C 541 | 12.4 | 42.8 | 44 | 6  | E55471    | E55471 Gene expres  | C 614 | 12.2 | 42.1 | 30 | 6  | E55294     | E55294 Novel metal   |
| C 542 | 12.4 | 42.8 | 44 | 6  | I21208    | I21208 Sequence 54  | 615   | 12.2 | 42.1 | 30 | 6  | I39990     | I39990 Sequence 43   |
| C 543 | 12.4 | 42.8 | 44 | 6  | I74475    | I74475 Sequence 54  | 616   | 12.2 | 42.1 | 30 | 6  | I40002     | I40002 Sequence 55   |
| C 544 | 12.4 | 42.8 | 45 | 6  | AX254647  | AX254647 Sequence   | C 617 | 12.2 | 42.1 | 30 | 6  | AR309877   | AR309877 Sequence    |
| C 545 | 12.4 | 42.8 | 46 | 6  | AX774021  | AX774021 Sequence   | C 618 | 12.2 | 42.1 | 30 | 6  | AR365714   | AR365714 Sequence    |
| C 546 | 12.4 | 42.8 | 46 | 6  | AX799825  | AX799825 Sequence   | C 619 | 12.2 | 42.1 | 30 | 6  | AX793354   | AX793354 Sequence    |
| C 547 | 12.4 | 42.8 | 47 | 6  | AR288904  | AR288904 Sequence   | 620   | 12.2 | 42.1 | 30 | 6  | BD166020   | BD166020 Method of   |
| C 548 | 12.4 | 42.8 | 47 | 6  | AR292024  | AR292024 Sequence   | C 621 | 12.2 | 42.1 | 31 | 6  | AX223485   | AX223485 Sequence    |
| C 549 | 12.4 | 42.8 | 48 | 6  | AR381024  | AR381024 Sequence   | C 622 | 12.2 | 42.1 | 31 | 6  | AX248729   | AX248729 Sequence    |
| C 550 | 12.4 | 42.8 | 48 | 6  | AX079966  | AX079966 Sequence   | C 623 | 12.2 | 42.1 | 32 | 6  | AR287881   | AR287881 Sequence    |
| C 551 | 12.4 | 42.8 | 48 | 6  | BD137448  | BD137448 Polymeras  | C 624 | 12.2 | 42.1 | 32 | 6  | AX236574   | AX236574 Sequence    |
| C 552 | 12.4 | 42.8 | 48 | 14 | SV40MKV1  | K00807 simian viru  | 625   | 12.2 | 42.1 | 32 | 6  | AX304420   | AX304420 Sequence    |
| C 553 | 12.4 | 42.8 | 49 | 6  | AX496194  | AX496194 Sequence   | 626   | 12.2 | 42.1 | 32 | 6  | AR151233   | AR151233 Sequence    |
| C 554 | 12.4 | 42.8 | 50 | 6  | AX162082  | AX162082 Sequence   | C 627 | 12.2 | 42.1 | 33 | 6  | BD107554   | BD107554 Nucleic a   |
| C 555 | 12.4 | 42.8 | 50 | 8  | AJ587185  | AJ587185 Arabidops  | 628   | 12.2 | 42.1 | 34 | 6  | BD276157   | BD276157 Recombina   |
| C 556 | 12.4 | 42.8 | 51 | 6  | AX115997  | AX115997 Sequence   | 629   | 12.2 | 42.1 | 34 | 6  | AR365647   | AR365647 Sequence    |
| C 557 | 12.4 | 42.8 | 51 | 6  | AX158567  | AX158567 Sequence   | 630   | 12.2 | 42.1 | 34 | 6  | BD166018   | BD166018 Method of   |
| C 558 | 12.4 | 42.8 | 51 | 6  | AX161425  | AX161425 Sequence   | 631   | 12.2 | 42.1 | 35 | 6  | A07726     | A07726 Oligonucleo   |
| C 559 | 12.4 | 42.8 | 51 | 6  | AX162081  | AX162081 Sequence   | 632   | 12.2 | 42.1 | 35 | 6  | A10025     | A10025 Nucleotide    |
| C 560 | 12.4 | 42.8 | 53 | 6  | AX494482  | AX494482 Sequence   | 633   | 12.2 | 42.1 | 36 | 6  | AR068015   | AR068015 Sequence    |
| C 561 | 12.4 | 42.8 | 54 | 6  | AX297550  | AX297550 Sequence   | 634   | 12.2 | 42.1 | 36 | 6  | AR120218   | AR120218 Sequence    |
| C 562 | 12.4 | 42.8 | 55 | 14 | APH0V1    | K01348 Foot and mo  | 635   | 12.2 | 42.1 | 36 | 6  | I57363     | I57363 Sequence 6    |
| C 563 | 12.4 | 42.8 | 56 | 8  | ATH524831 | AJ524831 Arabidops  | 636   | 12.2 | 42.1 | 37 | 6  | AX742083   | AX742083 Sequence    |
| C 564 | 12.4 | 42.8 | 60 | 6  | AX766039  | AX766039 Sequence   | 637   | 12.2 | 42.1 | 38 | 6  | AR045510   | AR045510 Sequence    |
| C 565 | 12.4 | 42.8 | 60 | 6  | AX776314  | AX776314 Sequence   | 638   | 12.2 | 42.1 | 38 | 6  | AR046016   | AR046016 Sequence    |
| C 566 | 12.4 | 42.8 | 62 | 8  | AJ588003  | AJ588003 Arabidops  | 639   | 12.2 | 42.1 | 38 | 6  | AR046084   | AR046084 Sequence    |
| C 567 | 12.4 | 42.8 | 63 | 8  | AJ589598  | AJ589598 Arabidops  | 640   | 12.2 | 42.1 | 38 | 6  | AR046535   | AR046535 Sequence    |
| C 568 | 12.4 | 42.8 | 65 | 6  | AR179429  | AR179429 Sequence   | 641   | 12.2 | 42.1 | 38 | 6  | I52562     | I52562 Sequence 30   |
| C 569 | 12.4 | 42.8 | 65 | 6  | AR205693  | AR205693 Sequence   | 642   | 12.2 | 42.1 | 38 | 6  | I53068     | I53068 Sequence 80   |
| C 570 | 12.4 | 42.8 | 65 | 6  | AX073548  | AX073548 Sequence   | 643   | 12.2 | 42.1 | 38 | 6  | I53136     | I53136 Sequence 87   |
| C 571 | 12.4 | 42.8 | 65 | 6  | AX482858  | AX482858 Sequence   | 644   | 12.2 | 42.1 | 38 | 6  | I53587     | I53587 Sequence 13   |
| C 572 | 12.4 | 42.8 | 65 | 6  | AX486452  | AX486452 Sequence   | 645   | 12.2 | 42.1 | 38 | 9  | S63153     | S63153 hprt-hypoxa   |
| C 573 | 12.4 | 42.8 | 66 | 1  | AF178301  | AF178301 Chlamydia  | 646   | 12.2 | 42.1 | 39 | 6  | A07727     | A07727 Oligonucleo   |
| C 574 | 12.4 | 42.8 | 66 | 1  | S6673951  | S66739 compl-major  | C 647 | 12.2 | 42.1 | 39 | 6  | A10026     | A10026 Nucleotide    |
| C 575 | 12.4 | 42.8 | 68 | 6  | AR356644  | AR356644 Sequence   | C 648 | 12.2 | 42.1 | 39 | 6  | E04800     | E04800 PCR primer    |
| C 576 | 12.4 | 42.8 | 71 | 6  | AX573330  | AX573330 Sequence   | C 649 | 12.2 | 42.1 | 39 | 6  | AR356667   | AR356667 Sequence    |

|       |      |      |    |    |           |                    |       |      |      |    |    |            |                     |
|-------|------|------|----|----|-----------|--------------------|-------|------|------|----|----|------------|---------------------|
| C 650 | 12.2 | 42.1 | 39 | 6  | BD061900  | BD061900 Antigenic | 723   | 12.2 | 42.1 | 54 | 6  | BD048253   | BD048253 Sequence   |
| C 651 | 12.2 | 42.1 | 40 | 6  | BD250819  | BD250819 Glycosyla | 724   | 12.2 | 42.1 | 54 | 8  | ATH523928  | ATH523928 Arabidops |
| C 652 | 12.2 | 42.1 | 40 | 6  | AR373200  | AR373200 Sequence  | 725   | 12.2 | 42.1 | 55 | 6  | AR102302   | AR102302 Sequence   |
| C 653 | 12.2 | 42.1 | 40 | 6  | BD107566  | BD107566 Nucleic a | 726   | 12.2 | 42.1 | 55 | 6  | AX683481   | AX683481 Sequence   |
| C 654 | 12.2 | 42.1 | 40 | 9  | HSZ78086  | Z78086 H.sapiens T | C 727 | 12.2 | 42.1 | 57 | 11 | HUMUTS347A | L30843 Human STS U  |
| C 655 | 12.2 | 42.1 | 41 | 6  | AR083451  | AR083451 Sequence  | 728   | 12.2 | 42.1 | 58 | 6  | AR420683   | AR420683 Sequence   |
| C 656 | 12.2 | 42.1 | 41 | 6  | AX514045  | AX514045 Sequence  | 729   | 12.2 | 42.1 | 58 | 6  | BD116236   | BD116236 EST and e  |
| C 657 | 12.2 | 42.1 | 41 | 6  | AX520514  | AX520514 Sequence  | C 730 | 12.2 | 42.1 | 59 | 6  | AR171509   | AR171509 Sequence   |
| C 658 | 12.2 | 42.1 | 41 | 6  | AX708349  | AX708349 Sequence  | C 731 | 12.2 | 42.1 | 59 | 6  | T25122     | T25122 Sequence 3   |
| C 659 | 12.2 | 42.1 | 41 | 6  | AX708363  | AX708363 Sequence  | C 732 | 12.2 | 42.1 | 59 | 6  | BD005529   | BD005529 Compositi  |
| C 660 | 12.2 | 42.1 | 41 | 6  | AX798427  | AX798427 Sequence  | C 733 | 12.2 | 42.1 | 62 | 6  | AX011399   | AX011399 Sequence   |
| C 661 | 12.2 | 42.1 | 42 | 6  | AR102301  | AR102301 Sequence  | 734   | 12.2 | 42.1 | 62 | 6  | BD225690   | BD225690 Screening  |
| C 662 | 12.2 | 42.1 | 42 | 6  | AX708344  | AX708344 Sequence  | C 735 | 12.2 | 42.1 | 63 | 6  | I09155     | I09155 Sequence 15  |
| C 663 | 12.2 | 42.1 | 42 | 6  | AX708358  | AX708358 Sequence  | 736   | 12.2 | 42.1 | 63 | 6  | AX708346   | AX708346 Sequence   |
| C 664 | 12.2 | 42.1 | 42 | 6  | AX798426  | AX798426 Sequence  | 737   | 12.2 | 42.1 | 63 | 6  | AX708360   | AX708360 Sequence   |
| C 665 | 12.2 | 42.1 | 43 | 6  | AX483394  | AX483394 Sequence  | C 738 | 12.2 | 42.1 | 63 | 9  | HSU91085   | U91085 Homo sapien  |
| C 666 | 12.2 | 42.1 | 43 | 6  | AX597814  | AX597814 Sequence  | C 739 | 12.2 | 42.1 | 63 | 9  | HSU91259   | U91259 Homo sapien  |
| C 667 | 12.2 | 42.1 | 43 | 6  | AX742082  | AX742082 Sequence  | 740   | 12.2 | 42.1 | 65 | 6  | A06240     | A06240 Synthetic H  |
| C 668 | 12.2 | 42.1 | 44 | 6  | AR063773  | AR063773 Sequence  | 741   | 12.2 | 42.1 | 65 | 6  | AX483879   | AX483879 Sequence   |
| C 669 | 12.2 | 42.1 | 44 | 6  | I30136    | I30136 Sequence 58 | 742   | 12.2 | 42.1 | 65 | 6  | AX485418   | AX485418 Sequence   |
| C 670 | 12.2 | 42.1 | 45 | 6  | A51851    | A51851 Sequence 15 | 743   | 12.2 | 42.1 | 65 | 6  | AX486471   | AX486471 Sequence   |
| C 671 | 12.2 | 42.1 | 45 | 6  | AR085824  | AR085824 Sequence  | 744   | 12.2 | 42.1 | 65 | 6  | AX486609   | AX486609 Sequence   |
| C 672 | 12.2 | 42.1 | 45 | 6  | AR093094  | AR093094 Sequence  | C 745 | 12.2 | 42.1 | 65 | 10 | AF357452   | AF357452 Mus muscu  |
| C 673 | 12.2 | 42.1 | 45 | 6  | AR099108  | AR099108 Sequence  | C 746 | 12.2 | 42.1 | 66 | 6  | AX288026   | AX288026 Arabidops  |
| C 674 | 12.2 | 42.1 | 47 | 6  | A07730    | A07730 Oligonucleo | C 747 | 12.2 | 42.1 | 67 | 8  | AJ596071   | AJ596071 Arabidops  |
| C 675 | 12.2 | 42.1 | 47 | 6  | AR284448  | AR284448 Sequence  | 748   | 12.2 | 42.1 | 67 | 14 | S57854S1   | S57854 Sigma virus  |
| C 676 | 12.2 | 42.1 | 47 | 6  | AR284640  | AR284640 Sequence  | 749   | 12.2 | 42.1 | 69 | 6  | AX920653   | AX920653 Sequence   |
| C 677 | 12.2 | 42.1 | 47 | 6  | AR290551  | AR290551 Sequence  | 750   | 12.2 | 42.1 | 69 | 6  | BD056186   | BD056186 Sequence   |
| C 678 | 12.2 | 42.1 | 47 | 6  | AR291223  | AR291223 Sequence  | 751   | 12.2 | 42.1 | 70 | 6  | AR054896   | AR054896 Sequence   |
| C 679 | 12.2 | 42.1 | 48 | 6  | A01761    | A01761 pT4-m DNA   | 752   | 12.2 | 42.1 | 70 | 6  | AR066161   | AR066161 Sequence   |
| C 680 | 12.2 | 42.1 | 48 | 6  | A15952    | A15952 Oligonucleo | 753   | 12.2 | 42.1 | 71 | 10 | MMU403504  | AJ403504 M.musculu  |
| C 681 | 12.2 | 42.1 | 48 | 6  | BD179481  | BD179481 Gene expr | 754   | 12.2 | 42.1 | 72 | 6  | AX694993   | AX694993 Sequence   |
| C 682 | 12.2 | 42.1 | 48 | 6  | BD188820  | BD188820 Gene expr | 755   | 12.2 | 42.1 | 72 | 6  | AX708350   | AX708350 Sequence   |
| C 683 | 12.2 | 42.1 | 49 | 6  | AX781482  | AX781482 Sequence  | 756   | 12.2 | 42.1 | 72 | 6  | AX708364   | AX708364 Sequence   |
| C 684 | 12.2 | 42.1 | 49 | 6  | AX816991  | AX816991 Sequence  | C 757 | 12.2 | 42.1 | 73 | 6  | AX597817   | AX597817 Sequence   |
| C 685 | 12.2 | 42.1 | 50 | 6  | AR164552  | AR164552 Sequence  | C 758 | 12.2 | 42.1 | 73 | 6  | AX597818   | AX597818 Sequence   |
| C 686 | 12.2 | 42.1 | 50 | 6  | AX160546  | AX160546 Sequence  | C 759 | 12.2 | 42.1 | 74 | 6  | AX096183   | AX096183 Sequence   |
| C 687 | 12.2 | 42.1 | 50 | 6  | AX160546  | AX160546 Sequence  | 760   | 12.2 | 42.1 | 75 | 7  | FT5PU5     | MI1608 Bacterioph   |
| C 688 | 12.2 | 42.1 | 50 | 6  | AX160756  | AX160756 Sequence  | C 761 | 12.2 | 42.1 | 76 | 6  | AR079098   | AR079098 Sequence   |
| C 689 | 12.2 | 42.1 | 50 | 6  | AX160968  | AX160968 Sequence  | C 762 | 12.2 | 42.1 | 78 | 6  | I34799     | I34799 Sequence 19  |
| C 690 | 12.2 | 42.1 | 51 | 1  | HIAGCC2   | Z33385 H.influenza | C 763 | 12.2 | 42.1 | 78 | 6  | I64517     | I64517 Sequence 19  |
| C 691 | 12.2 | 42.1 | 51 | 3  | S66469    | S66469 12S rRNA (p | 764   | 12.2 | 42.1 | 78 | 6  | AR420901   | AR420901 Sequence   |
| C 692 | 12.2 | 42.1 | 51 | 6  | A07731    | A07731 Oligonucleo | 765   | 12.2 | 42.1 | 78 | 6  | BD116454   | BD116454 EST and e  |
| C 693 | 12.2 | 42.1 | 51 | 6  | A10029    | A10029 Nucleotide  | C 766 | 12.2 | 42.1 | 80 | 6  | A51883     | A51883 Sequence 47  |
| C 694 | 12.2 | 42.1 | 51 | 6  | AR090925  | AR090925 Sequence  | C 767 | 12.2 | 42.1 | 80 | 6  | AR063776   | AR063776 Sequence   |
| C 695 | 12.2 | 42.1 | 51 | 6  | AR052680  | AR052680 Sequence  | C 768 | 12.2 | 42.1 | 80 | 6  | AR063777   | AR063777 Sequence   |
| C 696 | 12.2 | 42.1 | 51 | 6  | AR050991  | AR050991 Sequence  | 769   | 12.2 | 42.1 | 80 | 6  | AR085848   | AR085848 Sequence   |
| C 697 | 12.2 | 42.1 | 51 | 6  | AR057722  | AR057722 Sequence  | C 770 | 12.2 | 42.1 | 80 | 6  | I30139     | I30139 Sequence 61  |
| C 698 | 12.2 | 42.1 | 51 | 6  | AR175113  | AR175113 Sequence  | C 771 | 12.2 | 42.1 | 80 | 6  | I30140     | I30140 Sequence 62  |
| C 699 | 12.2 | 42.1 | 51 | 6  | I74699    | I74699 Sequence 39 | 772   | 12.2 | 42.1 | 80 | 6  | I30140     | I30140 Sequence     |
| C 700 | 12.2 | 42.1 | 51 | 6  | AR287993  | AR287993 Sequence  | C 773 | 12.2 | 42.1 | 18 | 6  | AX661812   | AX661812 Sequence   |
| C 701 | 12.2 | 42.1 | 51 | 6  | AR360127  | AR360127 Sequence  | C 774 | 12.2 | 42.1 | 19 | 6  | AX130174   | AX130174 Sequence   |
| C 702 | 12.2 | 42.1 | 51 | 6  | AR365606  | AR365606 Sequence  | 775   | 12.2 | 42.1 | 20 | 6  | AR100467   | AR100467 Sequence   |
| C 703 | 12.2 | 42.1 | 51 | 6  | AX115517  | AX115517 Sequence  | 776   | 12.2 | 42.1 | 20 | 6  | AR150122   | AR150122 Sequence   |
| C 704 | 12.2 | 42.1 | 51 | 6  | AX117933  | AX117933 Sequence  | 777   | 12.2 | 42.1 | 20 | 6  | BD227995   | BD227995 Antisense  |
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| C 818 | 12 | 41.4 | 40 | 12 | SYNREYSV2  | K01414 Ad2/SV40 de  | C 891 | 12   | 41.4 | 67 | 10 | RNU28644  | RNU28644 Rattus norv |
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## ALIGNMENTS

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DEFINITION Identification of molecular interaction sites in RNA for novel drug
ACCESSION BD274272
VERSION BD274272.1 GI:33084040
KEYWORDS JP 2002526030-A/239.
SOURCE synthetic construct

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ORGANISM synthetic construct
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AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE Identification of molecular interaction sites in RNA for novel drug
JOURNAL
COMMENT
OS PHARMACEUTICALS INC
PN JP 2002526030-A/239
PD 20-AUG-2002
PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
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Matches 20; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

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DEFINITION Identification of molecular interaction sites in RNA for novel drug
ACCESSION BD274273
VERSION BD274273.1 GI:33084041
KEYWORDS JP 2002526030-A/240.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 42)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE Identification of molecular interaction sites in RNA for novel drug
JOURNAL
COMMENT
OS PHARMACEUTICALS INC
PN JP 2002526030-A/240
PD 20-AUG-2002
PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
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ORIGIN
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RESULT 3
LOCUS BD274280 42 bp RNA linear PAT 17-JUL-2003
DEFINITION Identification of molecular interaction sites in RNA for novel drug
discovery.
ACCESSION BD274280
VERSION BD274280.1 GI:33084048
KEYWORDS JP 2002526030-A/247.
SOURCE synthetic construct
ORGANISM artificial construct
REFERENCE 1 (bases 1 to 42)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE Identification of molecular interaction sites in RNA for novel drug
discovery
JOURNAL Patent: JP 2002526030-A 247 20-AUG-2002;
COMMENT ISIS PHARMACEUTICALS INC
PN JP 2002526030-A/247
PD 20-AUG-2002
PF 12-MAY-1998 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC.
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ORIGIN
Query Match 100.0%; Score 29; DB 6; Length 42;
Best Local Similarity 69.0%; Pred. No. 0.0093;
Matches 20; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGAUUUUUUUAAGCCCAAGGGCU 29
    |||||:|||||:|||||:|||||:
Db 4 AAAGATTCTTTTGTAAAGCCCAAGGGCT 32

RESULT 4
LOCUS BD274281 42 bp RNA linear PAT 17-JUL-2003
DEFINITION Identification of molecular interaction sites in RNA for novel drug
discovery.
ACCESSION BD274281
VERSION BD274281.1 GI:33084049
KEYWORDS JP 2002526030-A/248.
SOURCE synthetic construct
ORGANISM artificial construct
REFERENCE 1 (bases 1 to 42)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE Identification of molecular interaction sites in RNA for novel drug
discovery
JOURNAL Patent: JP 2002526030-A 248 20-AUG-2002;
COMMENT ISIS PHARMACEUTICALS INC
PN JP 2002526030-A/248
PD 20-AUG-2002
PF 12-MAY-1998 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC

QY 1 AAAGAUUUUUUUAAGCCCAAGGGCU 29
    |||||:|||||:|||||:|||||:
Db 4 AAAGATTCTTTTGTAAAGCCCAAGGGCT 32

RESULT 5
LOCUS BD274241 46 bp DNA linear PAT 17-JUL-2003
DEFINITION Identification of molecular interaction sites in RNA for novel drug
discovery.
ACCESSION BD274241
VERSION BD274241.1 GI:33084009
KEYWORDS JP 2002526030-A/208.
SOURCE synthetic construct
ORGANISM artificial construct
REFERENCE 1 (bases 1 to 46)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE Identification of molecular interaction sites in RNA for novel drug
discovery
JOURNAL Patent: JP 2002526030-A 208 20-AUG-2002;
COMMENT ISIS PHARMACEUTICALS INC
PN JP 2002526030-A/208
PD 20-AUG-2002
PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
Cl2Q1/68,A61K31/7105,A61K48/00,Cl2N15/09,Cl2N15/00 CC Description
of Artificial Sequence: Novel Sequence FH Key
Location/Qualifiers
FT source 1..46
/organism='Artificial Sequence'.
FEATURES
source
1..46
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'
ORIGIN
Query Match 96.6%; Score 28; DB 6; Length 46;
Best Local Similarity 71.4%; Pred. No. 0.028;
Matches 20; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGAUUUUUUUAAGCCCAAGGGC 28
    |||||:|||||:|||||:|||||:
Db 19 AAAGATTCTTTTGTAAAGCCCAAGGGC 46

RESULT 6
LOCUS BD274242 46 bp DNA linear PAT 17-JUL-2003
DEFINITION Identification of molecular interaction sites in RNA for novel drug
discovery.
ACCESSION BD274242
VERSION BD274242.1 GI:33084010
KEYWORDS JP 2002526030-A/209.

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SOURCE      synthetic construct
ORGANISM    artificial sequences.
REFERENCE   1 (bases 1 to 46)
AUTHORS     Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE       Identification of molecular interaction sites in RNA for novel drug
            discovery
JOURNAL     Patent: JP 2002526030-A 209 20-AUG-2002;
COMMENT     ISIS PHARMACEUTICALS INC
OS          Artificial Sequence
PN          JP 2002526030-A/209
PD          20-AUG-2002
PF          12-MAY-1999 JP 2000548510
PR          12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
C1201/68 A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
Of Artificial Sequence: Novel Sequence FH Key
Location/Qualifiers
FT source 1..46
FT          Location/Qualifiers
FEATURES    source
            1..46
            /organism="synthetic construct"
            /mol_type="genomic DNA"
            /db_xref="taxon:32630"
ORIGIN
Query Match 96.6%; Score 28; DB 6; Length 46;
Best Local Similarity 71.4%; Pred. No. 0.028;
Matches 20; Conservative 8; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAAGAUUUUUUUUAAGCCCAAGGC 28
DB 19 AAAGATTCTTTTGTAAAGCCCAAGGC 46
RESULT 7
BD274243 46 bp DNA linear PAT 17-JUL-2003
LOCUS Identification of molecular interaction sites in RNA for novel drug
DEFINITION discovery.
ACCESSION BD274243.1 GI:33084011
VERSION JP 2002526030-A/210.
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 46)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE Identification of molecular interaction sites in RNA for novel drug
            discovery
JOURNAL Patent: JP 2002526030-A 210 20-AUG-2002;
COMMENT ISIS PHARMACEUTICALS INC
OS          Artificial Sequence
PN          JP 2002526030-A/210
PD          20-AUG-2002
PF          12-MAY-1999 JP 2000548510
PR          12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
C1201/68 A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
Of Artificial Sequence: Novel Sequence FH Key
Location/Qualifiers
FT source 1..46
FT          Location/Qualifiers
FEATURES    source
            1..46
            /organism="synthetic construct"
            /mol_type="genomic DNA"
            /db_xref="taxon:32630"
ORIGIN
Query Match 96.6%; Score 28; DB 6; Length 46;
Best Local Similarity 71.4%; Pred. No. 0.028;
Matches 20; Conservative 8; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAAGAUUUUUUUUAAGCCCAAGGC 28
DB 19 AAAGATTCTTTTGTAAAGCCCAAGGC 46

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Matches 20; Conservative 8; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAAGAUUUUUUUUAAGCCCAAGGC 28
DB 19 AAAGATTCTTTTGTAAAGCCCAAGGC 46
RESULT 8
BD274258 46 bp RNA linear PAT 17-JUL-2003
LOCUS Identification of molecular interaction sites in RNA for novel drug
DEFINITION discovery.
ACCESSION BD274258.1 GI:33084026
VERSION JP 2002526030-A/225.
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 46)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE Identification of molecular interaction sites in RNA for novel drug
            discovery
JOURNAL Patent: JP 2002526030-A 225 20-AUG-2002;
COMMENT ISIS PHARMACEUTICALS INC
OS          Artificial Sequence
PN          JP 2002526030-A/225
PD          20-AUG-2002
PF          12-MAY-1999 JP 2000548510
PR          12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
C1201/68 A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
Of Artificial Sequence: Novel Sequence FH Key
Location/Qualifiers
FT source 1..46
FT          Location/Qualifiers
FEATURES    source
            1..46
            /organism="synthetic construct"
            /mol_type="genomic RNA"
            /db_xref="taxon:32630"
ORIGIN
Query Match 96.6%; Score 28; DB 6; Length 46;
Best Local Similarity 71.4%; Pred. No. 0.028;
Matches 20; Conservative 8; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAAGAUUUUUUUUAAGCCCAAGGC 28
DB 19 AAAGATTCTTTTGTAAAGCCCAAGGC 46
RESULT 9
BD274259 46 bp RNA linear PAT 17-JUL-2003
LOCUS Identification of molecular interaction sites in RNA for novel drug
DEFINITION discovery.
ACCESSION BD274259.1 GI:33084027
VERSION JP 2002526030-A/226.
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 46)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE Identification of molecular interaction sites in RNA for novel drug
            discovery
JOURNAL Patent: JP 2002526030-A 226 20-AUG-2002;
COMMENT ISIS PHARMACEUTICALS INC
OS          Artificial Sequence
PN          JP 2002526030-A/226
PD          20-AUG-2002
PF          12-MAY-1999 JP 2000548510
PR          12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI

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Best Local Similarity 60.7%; Pred. No. 0.95; Mismatches 9; Indels 2; Gaps 0;
Matches 17; Conservative 9; Mismatches 9; Indels 2; Gaps 0;

Qy 2 AAGAUUCUUUUUGUAGCCCAAGGCU 29
|||||:|||||:|||||:|||||:
Db 5 AAGATTCTTTTGTAAAGCCCTACGGCT 32

RESULT 13
BD274238
LOCUS
DEFINITION Identification of molecular interaction sites in RNA for novel drug
discovery.
ACCESSION BD274238
VERSION BD274238.1 GI:33084006
KEYWORDS JP 2002526030-A/205.
SOURCE synthetic construct
ORGANISM artificial construct
REFERENCE 1 (bases 1 to 46)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE Identification of molecular interaction sites in RNA for novel drug
discovery.
JOURNAL Patent: JP 2002526030-A 205 20-AUG-2002;
COMMENT ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002526030-A/205
PD 20-AUG-2002
PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
C12Q1/68,A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
of Artificial Sequence: Novel Sequence FH Key
Location/Qualifiers
FT source 1..46
FT /organism='Artificial Sequence'.

FEATURES
source
1..46
Location/Qualifiers
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'

ORIGIN
Query Match 82.1%; Score 23.8; DB 6; Length 46;
Best Local Similarity 63.0%; Pred. No. 2.8;
Matches 17; Conservative 8; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AAGAUUCUUUUUGUAGCCCAAGGCU 28
|||||:|||||:|||||:|||||:
Db 20 AAGATTCTTTTGTAAAGCCCTACGGGC 46

RESULT 14
BD274238
LOCUS
DEFINITION Identification of molecular interaction sites in RNA for novel drug
discovery.
ACCESSION BD274238
VERSION BD274238.1 GI:33084004
KEYWORDS JP 2002526030-A/223.
SOURCE synthetic construct
ORGANISM artificial construct
REFERENCE 1 (bases 1 to 46)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE Identification of molecular interaction sites in RNA for novel drug
discovery.
JOURNAL Patent: JP 2002526030-A 223 20-AUG-2002;
COMMENT ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002526030-A/223
PD 20-AUG-2002
PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
C12Q1/68,A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
of Artificial Sequence: Novel Sequence FH Key
Location/Qualifiers
FT source 1..46
FT /organism='Artificial Sequence'.

FEATURES
source
1..46
Location/Qualifiers
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'

ORIGIN
Query Match 82.1%; Score 23.8; DB 6; Length 46;
Best Local Similarity 63.0%; Pred. No. 2.8;
Matches 17; Conservative 8; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AAGAUUCUUUUUGUAGCCCAAGGCU 28
|||||:|||||:|||||:|||||:
Db 20 AAGATTCTTTTGTAAAGCCCTACGGGC 46

RESULT 15
BD274275
LOCUS
DEFINITION Identification of molecular interaction sites in RNA for novel drug
discovery.
ACCESSION BD274275
VERSION BD274275.1 GI:33084043
KEYWORDS JP 2002526030-A/242.
SOURCE synthetic construct
ORGANISM artificial construct
REFERENCE 1 (bases 1 to 42)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE Identification of molecular interaction sites in RNA for novel drug
discovery.
JOURNAL Patent: JP 2002526030-A 242 20-AUG-2002;
COMMENT ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002526030-A/242
PD 20-AUG-2002
PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
C12Q1/68,A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
of Artificial Sequence: Novel Sequence FH Key
Location/Qualifiers
FT source 1..42
FT /organism='Artificial Sequence'.

FEATURES
source
1..42
Location/Qualifiers
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'

ORIGIN
Query Match 80.0%; Score 23.2; DB 6; Length 42;
Best Local Similarity 57.1%; Pred. No. 5.5;
Matches 16; Conservative 9; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AAGAUUCUUUUUGUAGCCCAAGGCU 29
|||||:|||||:|||||:|||||:
Db 5 ATGATTCTTTTGTAAAGCCCTAGGGCT 32

RESULT 16
BD274283
LOCUS
DEFINITION Identification of molecular interaction sites in RNA for novel drug
discovery.
ACCESSION BD274283
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PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
C12Q1/68,A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
of Artificial Sequence: Novel Sequence FH Key
Location/Qualifiers
FT source 1..46
FT /organism='Artificial Sequence'.

FEATURES
source
1..46
Location/Qualifiers
/organism='synthetic construct'
/mol_type='genomic RNA'
/db_xref='taxon:32630'

ORIGIN
Query Match 82.1%; Score 23.8; DB 6; Length 46;
Best Local Similarity 63.0%; Pred. No. 2.8;
Matches 17; Conservative 8; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AAGAUUCUUUUUGUAGCCCAAGGCU 28
|||||:|||||:|||||:|||||:
Db 20 AAGATTCTTTTGTAAAGCCCTACGGGC 46

RESULT 15
BD274275
LOCUS
DEFINITION Identification of molecular interaction sites in RNA for novel drug
discovery.
ACCESSION BD274275
VERSION BD274275.1 GI:33084043
KEYWORDS JP 2002526030-A/242.
SOURCE synthetic construct
ORGANISM artificial construct
REFERENCE 1 (bases 1 to 42)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE Identification of molecular interaction sites in RNA for novel drug
discovery.
JOURNAL Patent: JP 2002526030-A 242 20-AUG-2002;
COMMENT ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002526030-A/242
PD 20-AUG-2002
PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
C12Q1/68,A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
of Artificial Sequence: Novel Sequence FH Key
Location/Qualifiers
FT source 1..42
FT /organism='Artificial Sequence'.

FEATURES
source
1..42
Location/Qualifiers
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'

ORIGIN
Query Match 80.0%; Score 23.2; DB 6; Length 42;
Best Local Similarity 57.1%; Pred. No. 5.5;
Matches 16; Conservative 9; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AAGAUUCUUUUUGUAGCCCAAGGCU 29
|||||:|||||:|||||:|||||:
Db 5 ATGATTCTTTTGTAAAGCCCTAGGGCT 32

RESULT 16
BD274283
LOCUS
DEFINITION Identification of molecular interaction sites in RNA for novel drug
discovery.
ACCESSION BD274283
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VERSION      BD274283.1 GI:33084051
KEYWORDS     JP 2002526030-A/250.
SOURCE       synthetic construct
ORGANISM     artificial sequences.
REFERENCE     1 (bases 1 to 42)
AUTHORS      Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE        Identification of molecular interaction sites in RNA for novel drug
            discovery
JOURNAL      Patent: JP 2002526030-A 250 20-AUG-2002;
COMMENT      ISIS PHARMACEUTICALS INC
LOCUS        PN JP 2002526030-A/250
DEFINITION   PD 20-AUG-2002
ACCESSION    PF 12-MAY-1999 JP 2000548510
VERSION      PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
KEYWORDS     DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
SOURCE       C12Q1/68,A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
ORGANISM     of Artificial Sequence: Novel Sequence FH Key
REFERENCE     Location/Qualifiers
AUTHORS      FT source 1..42
TITLE        /organism='Artificial Sequence'.
JOURNAL      Location/Qualifiers
COMMENT      1..42
              /organism='synthetic construct'
              /mol_type='genomic RNA'
              /db_xref='taxon:32630'
ORIGIN
Query Match      80.0%; Score 23.2; DB 6; Length 42;
Best Local Similarity 57.1%; Pred. No. 5.5;
Matches 16; Conservative 9; Mismatches 3; Indels 0; Gaps 0;

QY      2 AAGAUUCUUUUUUAAGCCCAAGGGCU 29
        |||:|||||:|||||:|||||:
DB      5 ATGATTCCTTTTGTAGCCCTAGGGGCT 32
        |||:|||||:|||||:|||||:

RESULT 17
BD274240
LOCUS
DEFINITION   BD274240.1 GI:33084008
ACCESSION    JP 2002526030-A/207.
VERSION      synthetic construct
KEYWORDS     synthetic construct
SOURCE       artificial sequences.
REFERENCE     1 (bases 1 to 46)
AUTHORS      Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE        Identification of molecular interaction sites in RNA for novel drug
            discovery
JOURNAL      Patent: JP 2002526030-A 207 20-AUG-2002;
COMMENT      ISIS PHARMACEUTICALS INC
LOCUS        OS Artificial Sequence
DEFINITION   PN JP 2002526030-A/207
ACCESSION    PD 20-AUG-2002
VERSION      PF 12-MAY-1999 JP 2000548510
KEYWORDS     PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
SOURCE       DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
ORGANISM     C12Q1/68,A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
              of Artificial Sequence: Novel Sequence FH Key
              Location/Qualifiers
              FT source 1..46
              /organism='Artificial Sequence'.
              Location/Qualifiers
              1..46
              /organism='synthetic construct'
              /mol_type='genomic DNA'
              /db_xref='taxon:32630'
ORIGIN

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Query Match      76.6%; Score 22.2; DB 6; Length 46;
Best Local Similarity 59.3%; Pred. No. 17;
Matches 16; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY      2 AAGAUUCUUUUUUAAGCCCAAGGGC 28
        |||:|||||:|||||:|||||:
DB      20 ATGATTCCTTTTGTAGCCCTAGGGGC 46
        |||:|||||:|||||:|||||:

RESULT 18
BD274249
LOCUS
DEFINITION   BD274249.1 GI:33084017
ACCESSION    JP 2002526030-A/216.
VERSION      synthetic construct
KEYWORDS     synthetic construct
SOURCE       synthetic construct
ORGANISM     artificial sequences.
REFERENCE     1 (bases 1 to 46)
AUTHORS      Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE        Identification of molecular interaction sites in RNA for novel drug
            discovery
JOURNAL      Patent: JP 2002526030-A 216 20-AUG-2002;
COMMENT      ISIS PHARMACEUTICALS INC
LOCUS        OS Artificial Sequence
DEFINITION   PN JP 2002526030-A/216
ACCESSION    PD 20-AUG-2002
VERSION      PF 12-MAY-1999 JP 2000548510
KEYWORDS     PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
SOURCE       DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
ORGANISM     C12Q1/68,A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
              of Artificial Sequence: Novel Sequence FH Key
              Location/Qualifiers
              FT source 1..46
              /organism='Artificial Sequence'.
              Location/Qualifiers
              1..46
              /organism='synthetic construct'
              /mol_type='genomic DNA'
              /db_xref='taxon:32630'
ORIGIN
Query Match      76.6%; Score 22.2; DB 6; Length 46;
Best Local Similarity 59.3%; Pred. No. 17;
Matches 16; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY      2 AAGAUUCUUUUUUAAGCCCAAGGGC 28
        |||:|||||:|||||:|||||:
DB      20 ATGATTCCTTTTGTAGCCCTAGGGGC 46
        |||:|||||:|||||:|||||:

RESULT 19
BD274252
LOCUS
DEFINITION   BD274252.1 GI:33084020
ACCESSION    JP 2002526030-A/219.
VERSION      synthetic construct
KEYWORDS     synthetic construct
SOURCE       synthetic construct
ORGANISM     artificial sequences.
REFERENCE     1 (bases 1 to 46)
AUTHORS      Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE        Identification of molecular interaction sites in RNA for novel drug
            discovery
JOURNAL      Patent: JP 2002526030-A 219 20-AUG-2002;
COMMENT      ISIS PHARMACEUTICALS INC
LOCUS        OS Artificial Sequence
DEFINITION   PN JP 2002526030-A/219
ACCESSION    PD 20-AUG-2002

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PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
C12Q1/68,A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
of Artificial Sequence: Novel Sequence FH Key
Location/Qualifiers
PT source 1..46
FT /organism='Artificial Sequence'.

FEATURES
source
Location/Qualifiers
1..46
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match 76.6%; Score 22.2; DB 6; Length 46;
Best Local Similarity 59.3%; Pred. No. 17;
Matches 16; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY 2 AAGAUUUUUUGUAGGCCCAAGGGC 28
20 ATGATCTTTTGTAAAGCCCTAGGGC 46

Db

RESULT 20
BD274253 46 bp DNA linear PAT 17-JUL-2003
LOCUS Identification of molecular interaction sites in RNA for novel drug
DEFINITION discovery.
ACCESSION BD274253.1 GI:33084021
VERSION JP 2002526030-A/220.
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 46)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLES Identification of molecular interaction sites in RNA for novel drug
JOURNAL discovery
COMMENT Patent: JP 2002526030-A 220 20-AUG-2002;
ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002526030-A/220
PD 20-AUG-2002
PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
C12Q1/68,A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
of Artificial Sequence: Novel Sequence FH Key
Location/Qualifiers
PT source 1..46
FT /organism='Artificial Sequence'.

FEATURES
source
Location/Qualifiers
1..46
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match 76.6%; Score 22.2; DB 6; Length 46;
Best Local Similarity 59.3%; Pred. No. 17;
Matches 16; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY 2 AAGAUUUUUUGUAGGCCCAAGGGC 28
20 ATGATCTTTTGTAAAGCCCTAGGGC 46

Db

RESULT 21
BD274257 46 bp RNA linear PAT 17-JUL-2003
LOCUS Identification of molecular interaction sites in RNA for novel drug
DEFINITION discovery.
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ACCESSION BD274257
VERSION BD274257.1 GI:33084025
KEYWORDS JP 2002526030-A/224.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 46)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLES Identification of molecular interaction sites in RNA for novel drug
JOURNAL discovery
COMMENT Patent: JP 2002526030-A 224 20-AUG-2002;
ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002526030-A/224
PD 20-AUG-2002
PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
C12Q1/68,A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
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Location/Qualifiers
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FT /organism='Artificial Sequence'.

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Location/Qualifiers
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/mol_type="genomic RNA"
/db_xref="taxon:32630"

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Best Local Similarity 59.3%; Pred. No. 17;
Matches 16; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY 2 AAGAUUUUUUGUAGGCCCAAGGGC 28
20 ATGATCTTTTGTAAAGCCCTAGGGC 46

Db

RESULT 22
BD274265 46 bp RNA linear PAT 17-JUL-2003
LOCUS Identification of molecular interaction sites in RNA for novel drug
DEFINITION discovery.
ACCESSION BD274265.1 GI:33084033
VERSION JP 2002526030-A/232.
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 46)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLES Identification of molecular interaction sites in RNA for novel drug
JOURNAL discovery
COMMENT Patent: JP 2002526030-A 232 20-AUG-2002;
ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002526030-A/232
PD 20-AUG-2002
PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
C12Q1/68,A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
of Artificial Sequence: Novel Sequence FH Key
Location/Qualifiers
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source
Location/Qualifiers
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/mol_type="genomic RNA"
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ORIGIN
Query Match 76.6%; Score 22.2; DB 6; Length 46;
Best Local Similarity 59.3%; Pred. No. 17;
Matches 16; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY 2 AAGAUUUUUUGUAGGCCCAAGGGC 28
20 ATGATCTTTTGTAAAGCCCTAGGGC 46

Db

RESULT 23
BD274265 46 bp RNA linear PAT 17-JUL-2003
LOCUS Identification of molecular interaction sites in RNA for novel drug
DEFINITION discovery.
ACCESSION BD274265.1 GI:33084033
VERSION JP 2002526030-A/232.
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 46)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLES Identification of molecular interaction sites in RNA for novel drug
JOURNAL discovery
COMMENT Patent: JP 2002526030-A 232 20-AUG-2002;
ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002526030-A/232
PD 20-AUG-2002
PF 12-MAY-1999 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
C12Q1/68,A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description
of Artificial Sequence: Novel Sequence FH Key
Location/Qualifiers
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FT /organism='Artificial Sequence'.

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Location/Qualifiers
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/organism="synthetic construct"
/mol_type="genomic RNA"
/db_xref="taxon:32630"

ORIGIN
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discovery.
ACCESSION      BD274279
VERSION        BD274279.1  GI:33084047
KEYWORDS       JP 2002526030-A/246.
SOURCE         synthetic construct
ORGANISM       artificial construct
               artificial sequences.
REFERENCE      1 (bases 1 to 42)
AUTHORS       Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE         Identification of molecular interaction sites in RNA for novel drug
               discovery
JOURNAL       Patent: JP 2002526030-A 246 20-AUG-2002;
COMMENT       ISIS PHARMACEUTICALS INC
LOCUS         OS Artificial Sequence
               PN JP 2002526030-A/246
               PD 20-AUG-2002
               PF 12-MAY-1999 JP 2000548510
               PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
               KEYWORDS DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
               C1201/68 A61K31/7105 A61K48/00 C12N15/09 C12N15/00 CC Description
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/mol_type='genomic RNA'
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Best Local Similarity 57.7%; Pred. No. 50;
Matches 15; Conservative 8; Mismatches 3; Indels 0; Gaps 0;
QY 2 AGAUCUUUUUGUAGGCCCAAGG 27
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DB 5 AAGATCTTTTGTAGCCCTAGGCG 30
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RESULT 27
BD274247
LOCUS         46 bp DNA linear PAT 17-JUL-2003
DEFINITION   Identification of molecular interaction sites in RNA for novel drug
               discovery.
ACCESSION      BD274247
VERSION        BD274247.1  GI:33084015
KEYWORDS       JP 2002526030-A/214.
SOURCE         synthetic construct
ORGANISM       synthetic construct
               artificial sequences.
REFERENCE      1 (bases 1 to 46)
AUTHORS       Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE         Identification of molecular interaction sites in RNA for novel drug
               discovery
JOURNAL       Patent: JP 2002526030-A 214 20-AUG-2002;
COMMENT       ISIS PHARMACEUTICALS INC
LOCUS         OS Artificial Sequence
               PN JP 2002526030-A/214
               PD 20-AUG-2002
               PF 12-MAY-1999 JP 2000548510
               PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
               KEYWORDS DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
               C1201/68 A61K31/7105 A61K48/00 C12N15/09 C12N15/00 CC Description
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Location/Qualifiers
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ORIGIN
Query Match 73.1%; Score 21.2; DB 6; Length 46;
Best Local Similarity 57.7%; Pred. No. 50;
Matches 15; Conservative 8; Mismatches 3; Indels 0; Gaps 0;
QY 2 AGAUCUUUUUGUAGGCCCAAGG 27
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DB 20 AAGATCTTTTGTAGCCCTAGGCG 45
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RESULT 29
BD274237
LOCUS         46 bp DNA linear PAT 17-JUL-2003
DEFINITION   Identification of molecular interaction sites in RNA for novel drug
               discovery.
ACCESSION      BD274237
VERSION        BD274237.1  GI:33084005
KEYWORDS       JP 2002526030-A/204.
SOURCE         synthetic construct
ORGANISM       synthetic construct
               artificial sequences.
REFERENCE      1 (bases 1 to 46)
AUTHORS       Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE         Identification of molecular interaction sites in RNA for novel drug
               discovery
JOURNAL       Patent: JP 2002526030-A 204 20-AUG-2002;
COMMENT       ISIS PHARMACEUTICALS INC
LOCUS         OS Artificial Sequence
               PN JP 2002526030-A/204
               PD 20-AUG-2002
               PF 12-MAY-1999 JP 2000548510
               PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
               KEYWORDS DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
               C1201/68 A61K31/7105 A61K48/00 C12N15/09 C12N15/00 CC Description
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Location/Qualifiers
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Query Match 73.1%; Score 21.2; DB 6; Length 46;
Best Local Similarity 57.7%; Pred. No. 50;
Matches 15; Conservative 8; Mismatches 3; Indels 0; Gaps 0;
QY 2 AGAUCUUUUUGUAGGCCCAAGG 27
    |||||:|||||:|||||:|||||
DB 20 AAGATCTTTTGTAGCCCTAGGCG 45
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RESULT 28
BD274263
LOCUS         46 bp RNA linear PAT 17-JUL-2003
DEFINITION   Identification of molecular interaction sites in RNA for novel drug
               discovery.
ACCESSION      BD274263
VERSION        BD274263.1  GI:33084031
KEYWORDS       JP 2002526030-A/230.
SOURCE         synthetic construct
ORGANISM       synthetic construct
               artificial sequences.
REFERENCE      1 (bases 1 to 46)
AUTHORS       Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE         Identification of molecular interaction sites in RNA for novel drug
               discovery
JOURNAL       Patent: JP 2002526030-A 230 20-AUG-2002;
COMMENT       ISIS PHARMACEUTICALS INC
LOCUS         OS Artificial Sequence
               PN JP 2002526030-A/230
               PD 20-AUG-2002
               PF 12-MAY-1999 JP 2000548510
               PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
               KEYWORDS DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
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/mol_type='genomic RNA'
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Query Match 73.1%; Score 21.2; DB 6; Length 46;
Best Local Similarity 57.7%; Pred. No. 50;
Matches 15; Conservative 8; Mismatches 3; Indels 0; Gaps 0;
QY 2 AGAUCUUUUUGUAGGCCCAAGG 27
    |||||:|||||:|||||:|||||
DB 20 AAGATCTTTTGTAGCCCTAGGCG 45
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RESULT 29
BD274237
LOCUS         46 bp DNA linear PAT 17-JUL-2003
DEFINITION   Identification of molecular interaction sites in RNA for novel drug
               discovery.
ACCESSION      BD274237
VERSION        BD274237.1  GI:33084005
KEYWORDS       JP 2002526030-A/204.
SOURCE         synthetic construct
ORGANISM       synthetic construct
               artificial sequences.
REFERENCE      1 (bases 1 to 46)
AUTHORS       Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE         Identification of molecular interaction sites in RNA for novel drug
               discovery
JOURNAL       Patent: JP 2002526030-A 204 20-AUG-2002;
COMMENT       ISIS PHARMACEUTICALS INC
LOCUS         OS Artificial Sequence
               PN JP 2002526030-A/204
               PD 20-AUG-2002
               PF 12-MAY-1999 JP 2000548510
               PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
               KEYWORDS DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
               C1201/68 A61K31/7105 A61K48/00 C12N15/09 C12N15/00 CC Description
               of Artificial Sequence: Novel Sequence FH Key
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/mol_type='genomic DNA'
/db_xref='taxon:32630'
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Query Match 73.1%; Score 21.2; DB 6; Length 46;
Best Local Similarity 57.7%; Pred. No. 50;
Matches 15; Conservative 8; Mismatches 3; Indels 0; Gaps 0;
QY 2 AGAUCUUUUUGUAGGCCCAAGG 27
    |||||:|||||:|||||:|||||
DB 20 AAGATCTTTTGTAGCCCTAGGCG 45
    |||||:|||||:|||||:|||||

RESULT 28
BD274263
LOCUS         46 bp RNA linear PAT 17-JUL-2003
DEFINITION   Identification of molecular interaction sites in RNA for novel drug
               discovery.
ACCESSION      BD274263
VERSION        BD274263.1  GI:33084031
KEYWORDS       JP 2002526030-A/230.
SOURCE         synthetic construct
ORGANISM       synthetic construct
               artificial sequences.
REFERENCE      1 (bases 1 to 46)
AUTHORS       Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLE         Identification of molecular interaction sites in RNA for novel drug
               discovery
JOURNAL       Patent: JP 2002526030-A 230 20-AUG-2002;
COMMENT       ISIS PHARMACEUTICALS INC
LOCUS         OS Artificial Sequence
               PN JP 2002526030-A/230
               PD 20-AUG-2002
               PF 12-MAY-1999 JP 2000548510
               PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
               KEYWORDS DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
               C1201/68 A61K31/7105 A61K48/00 C12N15/09 C12N15/00 CC Description
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Query Match 73.1%; Score 21.2; DB 6; Length 46;
Best Local Similarity 57.7%; Pred. No. 50;
Matches 15; Conservative 8; Mismatches 3; Indels 0; Gaps 0;
QY 2 AGAUCUUUUUGUAGGCCCAAGG 27
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DB 20 AAGATCTTTTGTAGCCCTAGGCG 45
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PN JP 2002526030-A/204
PD 20-AUG-2002
PF 12-MAY-1998 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER, RANGA SAMPATH, RICHARD GRIFFEY, JOHN MCNEIL PC
C12Q1/68 A61K31/7105, A61K48/00, C12N15/09, C12N15/00 CC Description
of Artificial Sequence: Novel Sequence CC N is any nucleotide
FH Key Location/Qualifiers
FT misc feature (40)...(46).
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   /db_xref="taxon:32630"

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Query Match 69.0%; Score 20; DB 6; Length 46;
Best Local Similarity 60.0%; Pred. No. 1.9e+02;
Matches 12; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AAGAUUCUUUUGUAGGCC 21
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Db 20 AAGATTCCTTTTGTAGGCC 39

RESULT 30
BD274251 46 bp DNA linear PAT 17-JUL-2003
LOCUS
DEFINITION Identification of molecular interaction sites in RNA for novel drug
discovery.
ACCESSION BD274251
VERSION BD274251.1 GI:33084019
KEYWORDS JP 2002526030-A/218.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 46)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLES Identification of molecular interaction sites in RNA for novel drug
discovery
JOURNAL Patent: JP 2002526030-A 218 20-AUG-2002;
COMMENT ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002526030-A/218
PD 20-AUG-2002
PF 12-MAY-1998 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER, RANGA SAMPATH, RICHARD GRIFFEY, JOHN MCNEIL PC
C12Q1/68 A61K31/7105, A61K48/00, C12N15/09, C12N15/00 CC Description
of Artificial Sequence: Novel Sequence CC N is any nucleotide
FH Key Location/Qualifiers
FT misc feature (40)...(46).
   Location/Qualifiers
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   /mol_type="genomic DNA"
   /db_xref="taxon:32630"

ORIGIN
Query Match 69.0%; Score 20; DB 6; Length 46;
Best Local Similarity 60.0%; Pred. No. 1.9e+02;
Matches 12; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AAGAUUCUUUUGUAGGCC 21
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Db 20 AAGATTCCTTTTGTAGGCC 39

RESULT 31
BD274255 46 bp DNA linear PAT 17-JUL-2003
LOCUS
DEFINITION Identification of molecular interaction sites in RNA for novel drug
discovery.
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ACCESSION BD274255
VERSION BD274255.1 GI:33084023
KEYWORDS JP 2002526030-A/222.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 46)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLES Identification of molecular interaction sites in RNA for novel drug
discovery
JOURNAL Patent: JP 2002526030-A 222 20-AUG-2002;
COMMENT ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002526030-A/222
PD 20-AUG-2002
PF 12-MAY-1998 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER, RANGA SAMPATH, RICHARD GRIFFEY, JOHN MCNEIL PC
C12Q1/68 A61K31/7105, A61K48/00, C12N15/09, C12N15/00 CC Description
of Artificial Sequence: Novel Sequence CC N is any nucleotide
FH Key Location/Qualifiers
FT misc feature (40)...(46).
   Location/Qualifiers
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   /db_xref="taxon:32630"

ORIGIN
Query Match 69.0%; Score 20; DB 6; Length 46;
Best Local Similarity 60.0%; Pred. No. 1.9e+02;
Matches 12; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AAGAUUCUUUUGUAGGCC 21
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Db 20 AAGATTCCTTTTGTAGGCC 39

RESULT 32
BD274267 46 bp DNA linear PAT 17-JUL-2003
LOCUS
DEFINITION Identification of molecular interaction sites in RNA for novel drug
discovery.
ACCESSION BD274267
VERSION BD274267.1 GI:33084035
KEYWORDS JP 2002526030-A/234.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 46)
AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
TITLES Identification of molecular interaction sites in RNA for novel drug
discovery
JOURNAL Patent: JP 2002526030-A 234 20-AUG-2002;
COMMENT ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002526030-A/234
PD 20-AUG-2002
PF 12-MAY-1998 JP 2000548510
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI
DAVID J ECKER, RANGA SAMPATH, RICHARD GRIFFEY, JOHN MCNEIL PC
C12Q1/68 A61K31/7105, A61K48/00, C12N15/09, C12N15/00 CC Description
of Artificial Sequence: Novel Sequence CC N is any nucleotide
FH Key Location/Qualifiers
FT misc feature (40)...(46).
   Location/Qualifiers
   1..46
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ORIGIN
Query Match 69.0%; Score 20; DB 6; Length 46;
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Best Local Similarity 60.0%; Pred. No. 1.9e+02; Indels 0; Gaps 0;  
 Matches 12; Conservative 8; Mismatches 0;  
 QY 2 AAGAUUUUUUUAAGCC 21  
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 Db 20 AAGATCTTTGTAAGCC 39

RESULT 33  
 BD274284  
 LOCUS  
 DEFINITION Identification of molecular interaction sites in RNA for novel drug discovery.  
 ACCESSION BD274284  
 VERSION BD274284.1 GI:33084052  
 KEYWORDS JP 2002526030-A/251.  
 SOURCE synthetic construct  
 ORGANISM artificial sequences.  
 REFERENCE 1 (bases 1 to 42)  
 AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.  
 TITLE Identification of molecular interaction sites in RNA for novel drug discovery  
 JOURNAL Patent: JP 2002526030-A 251 20-AUG-2002;  
 COMMENT ISIS PHARMACEUTICALS INC  
 OS Artificial Sequence  
 PN JP 2002526030-A/251  
 PD 20-AUG-2002  
 PF 12-MAY-1999 JP 2000548510  
 PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI  
 DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC  
 C12Q1/68,A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description  
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 Location/Qualifiers  
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 FT Location/Qualifiers

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 /mol\_type="genomic RNA"  
 /db\_xref="taxon:32630"

ORIGIN

Query Match 67.6%; Score 19.6; DB 6; Length 42;  
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 Matches 15; Conservative 7; Mismatches 4; Indels 0; Gaps 0;  
 QY 4 GAUUCUUUUUUAAGCCCAAGGCCU 29  
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 Db 7 GATCCTTTCTGTAGCCCTACGGCT 32

RESULT 34  
 BD274246  
 LOCUS  
 DEFINITION Identification of molecular interaction sites in RNA for novel drug discovery.  
 ACCESSION BD274246  
 VERSION BD274246.1 GI:33084014  
 KEYWORDS JP 2002526030-A/213.  
 SOURCE synthetic construct  
 ORGANISM artificial sequences.  
 REFERENCE 1 (bases 1 to 46)  
 AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.  
 TITLE Identification of molecular interaction sites in RNA for novel drug discovery  
 JOURNAL Patent: JP 2002526030-A 213 20-AUG-2002;  
 COMMENT ISIS PHARMACEUTICALS INC  
 OS Artificial Sequence  
 PN JP 2002526030-A/213  
 PD 20-AUG-2002  
 PF 12-MAY-1999 JP 2000548510

PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI  
 DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC  
 C12Q1/68,A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC Description  
 of Artificial Sequence: Novel Sequence FH Key  
 Location/Qualifiers  
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 FT /organism='Artificial Sequence'.  
 FT Location/Qualifiers

FEATURES  
 source

1..46  
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 /mol\_type="genomic DNA"  
 /db\_xref="taxon:32630"

ORIGIN

Query Match 64.1%; Score 18.6; DB 6; Length 46;  
 Best Local Similarity 60.0%; Pred. No. 8.7e+02;  
 Matches 15; Conservative 6; Mismatches 4; Indels 0; Gaps 0;  
 QY 4 GAUUCUUUUUUAAGCCCAAGGCC 28  
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 Db 22 GATCCTTTCTGTAGCCCTACGGCC 46

RESULT 35  
 BD274248  
 LOCUS  
 DEFINITION Identification of molecular interaction sites in RNA for novel drug discovery.  
 ACCESSION BD274248  
 VERSION BD274248.1 GI:33084016  
 KEYWORDS JP 2002526030-A/215.  
 SOURCE synthetic construct  
 ORGANISM artificial sequences.  
 REFERENCE 1 (bases 1 to 46)  
 AUTHORS Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.  
 TITLE Identification of molecular interaction sites in RNA for novel drug discovery  
 JOURNAL Patent: JP 2002526030-A 215 20-AUG-2002;  
 COMMENT ISIS PHARMACEUTICALS INC  
 OS Artificial Sequence  
 PN JP 2002526030-A/215  
 PD 20-AUG-2002  
 PF 12-MAY-1999 JP 2000548510  
 PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI  
 DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC  
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 of Artificial Sequence: Novel Sequence FH Key  
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FEATURES  
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 QY 4 GAUUCUUUUUUAAGCCCAAGGCC 28  
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 Db 22 GATCCTTTCTGTAGCCCTACGGCC 46

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 DEFINITION Identification of molecular interaction sites in RNA for novel drug discovery.  
 ACCESSION BD274262

[illegible]

PF 12-MAY-1999 JP 2000548510  
PR 12-MAY-1998 US 60/085092,12-MAY-1998 US 09/076440 PI  
DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFITHY,JOHN MCNEIL PC  
C12Q1/68,A6IK31/7105,A6IK48/00,C12N15/09,C12N15/00 CC Description  
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RESULT 40

ATH553793  
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DEFINITION Arabidopsis thaliana T-DNA flanking sequence, left border, clone 383B09.  
ACCESSION AJ553793  
VERSION AJ553793.1 GI:29370260  
KEYWORDS left border; T-DNA flanking sequence.  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana

REFERENCE

AUTHORS Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, P., Chauvin, S., Bechtold, N., Cruaud, C., Derose, R., Peilleter, G., Lepiniec, L., Caboche, M. and Lecharny, A.  
TITLE T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites  
JOURNAL EMBO Rep. 3 (12), 1152-1157 (2002)  
MEDLINE 22363535  
PUBMED 12446565  
AUTHORS Balzergue, S.  
TITLE Direct Submission  
JOURNAL Submitted (21-NOV-2002) Balzergue S., UMRGV, INRA/CNRS, 2 rue Gaston Crémieux, 91057 Evry cedex, FRANCE

COMMENT

PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (<http://www.genoplante.com> and <http://genoplante-info.intobiogen.fr/>).  
Location/Qualifiers  
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source

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ORIGIN

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Db 2 AAAAATTCCTTTTGTAGGCATCAATGC 29

Search completed: April 18, 2004, 08:41:37  
Job time : 760.333 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 18, 2004; 05:05:34 ; Search time 179.667 Seconds  
(without alignments)

685.702 Million cell updates/sec

Title: US-09-310-844C-24

Perfect score: 29

Sequence: 1 uaugauuuuuuuaagccuaggggcu 29

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 337363 seqs, 212409041 residues

Total number of hits satisfying chosen parameters: 3399856

Minimum DB seq length: 0

Maximum DB seq length: 80

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

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9: geneseqn2003cs:\*

10: geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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| 98  | 14.2 | 49.0 | 51 | 8 | AD94846   | Primer P0 | 171   | 13.4 | 46.2 | 26 | 4 | AAH20991  | Aah20991  | C-myc epi |
| 99  | 14.2 | 49.0 | 56 | 4 | AD16838   | E. coli e | c 172 | 13.4 | 46.2 | 26 | 5 | AAC50401  | Rac90401  | Rat alpha |
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| 102 | 14   | 48.3 | 30 | 4 | AAF6581   | BmNPV PCR | c 175 | 13.4 | 46.2 | 30 | 6 | ABX67133  | Novel Hel | Abx67133  |
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| 107 | 14   | 48.3 | 41 | 6 | ABK11369  | NADH dehy | 180   | 13.4 | 46.2 | 41 | 2 | AAV08972  | PCR prime | Aav08972  |
| 108 | 14   | 48.3 | 44 | 2 | AAQ78588  | Vector am | 181   | 13.4 | 46.2 | 41 | 5 | AAI67146  | B. lichen | Aai67146  |
| 109 | 14   | 48.3 | 44 | 2 | AAQ78087  | Vector am | 182   | 13.4 | 46.2 | 42 | 2 | AAV29708  | PCR prime | Aav29708  |
| 110 | 14   | 48.3 | 60 | 6 | ABQ78142  | Synthetic | c 183 | 13.4 | 46.2 | 47 | 4 | AAH88296  | CNS disor | Aah88296  |
| 111 | 14   | 48.3 | 60 | 6 | ABN39439  | Human spl | c 184 | 13.4 | 46.2 | 47 | 6 | ABK40908  | Human obe | Abk40908  |
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| 113 | 14   | 48.3 | 62 | 3 | AAK11187  | Human sec | c 186 | 13.4 | 46.2 | 50 | 6 | ABZ05954  | Human leu | Abz05954  |
| 114 | 13.8 | 47.6 | 17 | 6 | AB874757  | Human PAP | c 187 | 13.4 | 46.2 | 50 | 6 | ABZ04409  | Human leu | Abz04409  |
| 115 | 13.8 | 47.6 | 25 | 6 | ABN97740  | Human XED | c 188 | 13.4 | 46.2 | 51 | 2 | AAQ31679  | Sheep LfA | Aaq31679  |
| 116 | 13.8 | 47.6 | 25 | 6 | AB875579  | Human PAP | c 189 | 13.4 | 46.2 | 51 | 2 | AAQ70412  | Sheep LfA | Aaq70412  |
| 117 | 13.8 | 47.6 | 25 | 6 | AB875580  | Human PAP | c 190 | 13.4 | 46.2 | 51 | 2 | AAV38551  | Ovine cel | Aav38551  |
| 118 | 13.8 | 47.6 | 25 | 8 | ACT08818  | Human mic | c 191 | 13.4 | 46.2 | 52 | 2 | AAV69331  | Human LIR | Aav69331  |
| 119 | 13.8 | 47.6 | 25 | 8 | ACT82368  | Human mic | c 192 | 13.4 | 46.2 | 52 | 3 | AA454594  | Primer ce | Aa454594  |
| 120 | 13.8 | 47.6 | 25 | 8 | ACH65059  | DNA tagge | c 193 | 13.4 | 46.2 | 54 | 6 | AAAL45748 | Cancer ce | Aal45748  |
| 121 | 13.8 | 47.6 | 30 | 6 | ABK14828  | Rat FGF-R | c 194 | 13.4 | 46.2 | 56 | 7 | ABZ79096  | Tumour su | Abz79096  |
| 122 | 13.8 | 47.6 | 31 | 6 | ABK21707  | Human ERG | c 195 | 13.4 | 46.2 | 56 | 7 | ABZ09643  | Human o11 | Abz09643  |
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| 124 | 13.8 | 47.6 | 36 | 3 | AA458448  | Cystathio | c 197 | 13.4 | 46.2 | 60 | 6 | ABN39064  | Human spl | Abn39064  |
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| 131 | 13.8 | 47.6 | 60 | 6 | ABN33773  | Human spl | c 204 | 13.2 | 45.5 | 25 | 8 | ACI76453  | Human mic | Act76453  |
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| 143 | 13.6 | 46.9 | 40 | 9 | ADB37733  | ALDI/ALD2 | c 216 | 13.2 | 45.5 | 27 | 2 | AAZ24804  | Downstrea | Aaz24804  |
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| 145 | 13.6 | 46.9 | 47 | 3 | AAZ68495  | Human map | c 218 | 13.2 | 45.5 | 27 | 2 | AAZ37444  | Synthetic | Aaz37444  |
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| 147 | 13.6 | 46.9 | 50 | 4 | AAI76933  | Human sil | c 220 | 13.2 | 45.5 | 27 | 2 | AAZ51694  | 3' PCR pr | Aaz51694  |
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| 154 | 13.6 | 46.9 | 60 | 6 | ABN35687  | Human spl | c 227 | 13.2 | 45.5 | 27 | 2 | AAV84404  | Downstrea | Aav84404  |
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| 162 | 13.6 | 46.9 | 66 | 6 | ABK97773  | C. tracho | c 235 | 13.2 | 45.5 | 27 | 2 | AAZ27304  | SV40 earl | Aaz27304  |
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| 166 | 13.4 | 46.2 | 25 | 8 | ACI51522  | Human mic | c 239 | 13.2 | 45.5 | 27 | 3 | AAC78451  | Downstrea | Aac78451  |
| 167 | 13.4 | 46.2 | 25 | 8 | ACK06797  | Human mic | c 240 | 13.2 | 45.5 | 27 | 3 | AAC59328  | SV40 prom | Aac59328  |
| 168 | 13.4 | 46.2 | 25 | 8 | ACI37325  | Human mic | c 241 | 13.2 | 45.5 | 27 | 3 | AAC74389  | Downstrea | Aac74389  |
| 169 | 13.4 | 46.2 | 26 | 3 | AAA30138  | Reverse P | c 242 | 13.2 | 45.5 | 27 | 3 | AAC67624  | Downstrea | Aac67624  |

|     |      |      |    |   |          |            |     |      |      |    |   |          |           |           |
|-----|------|------|----|---|----------|------------|-----|------|------|----|---|----------|-----------|-----------|
| 243 | 13.2 | 45.5 | 27 | 3 | AAC68074 | Downstrea  | 316 | 13.2 | 45.5 | 27 | 3 | AAC81703 | Aac81703  | GAS repor |
| 244 | 13.2 | 45.5 | 27 | 3 | AAC95514 | Downstrea  | 317 | 13.2 | 45.5 | 27 | 3 | AAC66218 | Aac66218  | Upstream  |
| 245 | 13.2 | 45.5 | 27 | 3 | AAC93472 | Downstrea  | 318 | 13.2 | 45.5 | 27 | 3 | AAC66223 | Aac66223  | Upstream  |
| 246 | 13.2 | 45.5 | 27 | 3 | AAC59500 | Downstrea  | 319 | 13.2 | 45.5 | 27 | 3 | AAC22309 | Aat22309  | Downstrea |
| 247 | 13.2 | 45.5 | 27 | 3 | AAC66403 | GAS repor  | 320 | 13.2 | 45.5 | 27 | 3 | AAC57525 | Aas57525  | PCR prime |
| 248 | 13.2 | 45.5 | 27 | 3 | AAC58983 | GAS repor  | 321 | 13.2 | 45.5 | 27 | 3 | AAC57530 | Aas57530  | PCR prime |
| 249 | 13.2 | 45.5 | 27 | 3 | AAC58731 | Downstrea  | 322 | 13.2 | 45.5 | 27 | 3 | AAC59811 | Aas59811  | Downstrea |
| 250 | 13.2 | 45.5 | 27 | 3 | AAC98766 | Downstrea  | 323 | 13.2 | 45.5 | 27 | 3 | AAA50011 | AAA50011  | SV40 earl |
| 251 | 13.2 | 45.5 | 27 | 3 | AAA61253 | Downstrea  | 324 | 13.2 | 45.5 | 27 | 3 | AAA59229 | Aas59229  | PCR prime |
| 252 | 13.2 | 45.5 | 27 | 3 | AAF22034 | Downstrea  | 325 | 13.2 | 45.5 | 27 | 3 | AAA59208 | Aas59208  | Downstrea |
| 253 | 13.2 | 45.5 | 27 | 3 | AAC93303 | Downstrea  | 326 | 13.2 | 45.5 | 27 | 3 | AA773849 | Aaa773849 | SV40 earl |
| 254 | 13.2 | 45.5 | 27 | 3 | AAA50319 | SV40 prom  | 327 | 13.2 | 45.5 | 27 | 3 | AAA74405 | Aaa74405  | SV40 earl |
| 255 | 13.2 | 45.5 | 27 | 3 | AA50325  | SV40 prom  | 328 | 13.2 | 45.5 | 27 | 3 | AAC69505 | Aad69505  | Downstrea |
| 256 | 13.2 | 45.5 | 27 | 3 | AAC59042 | GAS repor  | 329 | 13.2 | 45.5 | 27 | 3 | AD02080  | Aad02080  | Downstrea |
| 257 | 13.2 | 45.5 | 27 | 3 | AAC79674 | Downstrea  | 330 | 13.2 | 45.5 | 27 | 3 | AAC73858 | Aac73858  | Downstrea |
| 258 | 13.2 | 45.5 | 27 | 3 | AAC59385 | SV40 prom  | 331 | 13.2 | 45.5 | 27 | 3 | AAF22366 | Aaf22366  | Downstrea |
| 259 | 13.2 | 45.5 | 27 | 3 | AAZ36850 | 3', end of | 332 | 13.2 | 45.5 | 27 | 3 | AD02232  | Aad02232  | SV40 prom |
| 260 | 13.2 | 45.5 | 27 | 3 | AAZ36844 | PCR prime  | 333 | 13.2 | 45.5 | 27 | 4 | AAF33206 | Aaf33206  | Downstrea |
| 261 | 13.2 | 45.5 | 27 | 3 | AAA26339 | Downstrea  | 334 | 13.2 | 45.5 | 27 | 4 | AAF91851 | Aaf91851  | SV40 prom |
| 262 | 13.2 | 45.5 | 27 | 3 | AAC69448 | Downstrea  | 335 | 13.2 | 45.5 | 27 | 4 | AA502388 | Aas02388  | SV40 prom |
| 263 | 13.2 | 45.5 | 27 | 3 | AAC79733 | Downstrea  | 336 | 13.2 | 45.5 | 27 | 4 | AA523887 | Aaf23887  | SV40 prom |
| 264 | 13.2 | 45.5 | 27 | 3 | AAC59672 | SV40 prom  | 337 | 13.2 | 45.5 | 27 | 4 | AD05213  | Aad05213  | SV40 prom |
| 265 | 13.2 | 45.5 | 27 | 3 | AZ49756  | 3' PCR pri | 338 | 13.2 | 45.5 | 27 | 4 | AD05114  | Aad05114  | SV40 prom |
| 266 | 13.2 | 45.5 | 27 | 3 | AAZ49762 | Downstrea  | 339 | 13.2 | 45.5 | 27 | 4 | AD16728  | Aad16728  | SV40 prom |
| 267 | 13.2 | 45.5 | 27 | 3 | AAC59270 | SV40 prom  | 340 | 13.2 | 45.5 | 27 | 4 | AA198560 | Aai198560 | Downstrea |
| 268 | 13.2 | 45.5 | 27 | 3 | AAC59959 | Downstrea  | 341 | 13.2 | 45.5 | 27 | 4 | AAH46818 | Aah46818  | GAS-SV40  |
| 269 | 13.2 | 45.5 | 27 | 3 | AAZ78990 | Downstrea  | 342 | 13.2 | 45.5 | 27 | 4 | AA528929 | Aas28929  | Downstrea |
| 270 | 13.2 | 45.5 | 27 | 3 | AAC78460 | SV40 prom  | 343 | 13.2 | 45.5 | 27 | 4 | AA530354 | Aas30354  | PCR prime |
| 271 | 13.2 | 45.5 | 27 | 3 | AA805959 | Downstrea  | 344 | 13.2 | 45.5 | 27 | 4 | AAH26240 | Aah26240  | SV40 earl |
| 272 | 13.2 | 45.5 | 27 | 3 | AAA78374 | Downstrea  | 345 | 13.2 | 45.5 | 27 | 4 | AD20611  | Aad20611  | SV40 prom |
| 273 | 13.2 | 45.5 | 27 | 3 | AAA46742 | Primer fo  | 346 | 13.2 | 45.5 | 27 | 4 | AA81780  | Aaf81780  | Downstrea |
| 274 | 13.2 | 45.5 | 27 | 3 | AAZ98010 | SV40 prom  | 347 | 13.2 | 45.5 | 27 | 4 | AS01453  | Aas01453  | SV40 prom |
| 275 | 13.2 | 45.5 | 27 | 3 | AAC69590 | Downstrea  | 348 | 13.2 | 45.5 | 27 | 4 | AD05046  | Aad05046  | SV40 prom |
| 276 | 13.2 | 45.5 | 27 | 3 | AAC69077 | Downstrea  | 349 | 13.2 | 45.5 | 27 | 4 | AD07802  | Aad07802  | SV40 prom |
| 277 | 13.2 | 45.5 | 27 | 3 | AAC68018 | Downstrea  | 350 | 13.2 | 45.5 | 27 | 4 | AS11747  | Aas11747  | PCR prime |
| 278 | 13.2 | 45.5 | 27 | 3 | AAC93357 | Downstrea  | 351 | 13.2 | 45.5 | 27 | 4 | AA527607 | Aas27607  | Novel sig |
| 279 | 13.2 | 45.5 | 27 | 3 | AAA95094 | Downstrea  | 352 | 13.2 | 45.5 | 27 | 4 | AS11464  | Aas11464  | PCR prime |
| 280 | 13.2 | 45.5 | 27 | 3 | AA15755  | SV40 prom  | 353 | 13.2 | 45.5 | 27 | 4 | AA527599 | Aas27599  | Novel sig |
| 281 | 13.2 | 45.5 | 27 | 3 | AZ58632  | SV40 earl  | 354 | 13.2 | 45.5 | 27 | 4 | AA527602 | Aas27602  | Novel sig |
| 282 | 13.2 | 45.5 | 27 | 3 | AZ58626  | SV40 earl  | 355 | 13.2 | 45.5 | 27 | 4 | AA527603 | Aas27603  | Novel sig |
| 283 | 13.2 | 45.5 | 27 | 3 | AZ65243  | Downstrea  | 356 | 13.2 | 45.5 | 27 | 4 | AA527600 | Aas27600  | Novel sig |
| 284 | 13.2 | 45.5 | 27 | 3 | AAZ74216 | Downstrea  | 357 | 13.2 | 45.5 | 27 | 4 | AA527605 | Aas27605  | Novel sig |
| 285 | 13.2 | 45.5 | 27 | 3 | AA15508  | Downstrea  | 358 | 13.2 | 45.5 | 27 | 4 | AA527604 | Aas27604  | Novel sig |
| 286 | 13.2 | 45.5 | 27 | 3 | AAZ59617 | Downstrea  | 359 | 13.2 | 45.5 | 27 | 4 | AA527601 | Aas27601  | Novel sig |
| 287 | 13.2 | 45.5 | 27 | 3 | AAZ50694 | Downstrea  | 360 | 13.2 | 45.5 | 27 | 4 | AA527606 | Aas27606  | Novel sig |
| 288 | 13.2 | 45.5 | 27 | 3 | AAC79792 | Downstrea  | 361 | 13.2 | 45.5 | 27 | 4 | AA12416  | Aad12416  | PCR prime |
| 289 | 13.2 | 45.5 | 27 | 3 | AAC59559 | Downstrea  | 362 | 13.2 | 45.5 | 27 | 4 | AD16520  | Aad16520  | SV40 prom |
| 290 | 13.2 | 45.5 | 27 | 3 | AD00079  | 3', primer | 363 | 13.2 | 45.5 | 27 | 4 | ABK41606 | Abk41606  | Downstrea |
| 291 | 13.2 | 45.5 | 27 | 3 | AA18427  | Downstrea  | 364 | 13.2 | 45.5 | 27 | 4 | ABK03110 | Abk03110  | Downstrea |
| 292 | 13.2 | 45.5 | 27 | 3 | AAZ59442 | Downstrea  | 365 | 13.2 | 45.5 | 27 | 4 | AD20022  | Aad20022  | SV40 prom |
| 293 | 13.2 | 45.5 | 27 | 3 | AAC69392 | Downstrea  | 366 | 13.2 | 45.5 | 27 | 4 | AAZ91259 | Aac91259  | SV40 prom |
| 294 | 13.2 | 45.5 | 27 | 3 | AAZ97012 | SV40 prom  | 367 | 13.2 | 45.5 | 27 | 4 | AAZ72734 | Aaf72734  | Downstrea |
| 295 | 13.2 | 45.5 | 27 | 3 | AAA26274 | Downstrea  | 368 | 13.2 | 45.5 | 27 | 4 | AA500502 | Aas00502  | SV40 prom |
| 296 | 13.2 | 45.5 | 27 | 3 | AAA39045 | Downstrea  | 369 | 13.2 | 45.5 | 27 | 4 | AD05293  | Aad05293  | SV40 prom |
| 297 | 13.2 | 45.5 | 27 | 3 | AAC99234 | Downstrea  | 370 | 13.2 | 45.5 | 27 | 4 | AA12926  | Aas12926  | Human car |
| 298 | 13.2 | 45.5 | 27 | 3 | AAZ74273 | Downstrea  | 371 | 13.2 | 45.5 | 27 | 4 | ABK06875 | Abk06875  | SV40 prom |
| 299 | 13.2 | 45.5 | 27 | 3 | AAZ80524 | Downstrea  | 372 | 13.2 | 45.5 | 27 | 4 | AA540778 | Aas40778  | Downstrea |
| 300 | 13.2 | 45.5 | 27 | 3 | AAZ81079 | Downstrea  | 373 | 13.2 | 45.5 | 27 | 4 | AA540778 | Aas40778  | Human cyt |
| 301 | 13.2 | 45.5 | 27 | 3 | AAZ37782 | PCR prime  | 374 | 13.2 | 45.5 | 27 | 4 | AA511959 | Aas11959  | Human PCR |
| 302 | 13.2 | 45.5 | 27 | 3 | AAZ37777 | PCR prime  | 375 | 13.2 | 45.5 | 27 | 4 | AA511952 | Aas11952  | SV40 PCR  |
| 303 | 13.2 | 45.5 | 27 | 3 | AAC59900 | Downstrea  | 376 | 13.2 | 45.5 | 27 | 4 | AD16495  | Aad16495  | SV40 prom |
| 304 | 13.2 | 45.5 | 27 | 3 | AAZ59101 | GAS repor  | 377 | 13.2 | 45.5 | 27 | 4 | AD02746  | Aad02746  | GAS-SV40  |
| 305 | 13.2 | 45.5 | 27 | 3 | AAZ89976 | SV40 earl  | 378 | 13.2 | 45.5 | 27 | 4 | AAZ97877 | Aaf97877  | SV40 prom |
| 306 | 13.2 | 45.5 | 27 | 3 | AAC98893 | SV40 prom  | 379 | 13.2 | 45.5 | 27 | 4 | AD16776  | Aad16776  | Human nov |
| 307 | 13.2 | 45.5 | 27 | 3 | AAZ98985 | SV40 earl  | 380 | 13.2 | 45.5 | 27 | 4 | AD16743  | Aad16743  | SV40 prom |
| 308 | 13.2 | 45.5 | 27 | 3 | AAC93415 | Downstrea  | 381 | 13.2 | 45.5 | 27 | 4 | AA530582 | Aas30582  | PCR prime |
| 309 | 13.2 | 45.5 | 27 | 3 | AAC63403 | GAS repor  | 382 | 13.2 | 45.5 | 27 | 4 | AAH7444  | Aah7444   | SV40 earl |
| 310 | 13.2 | 45.5 | 27 | 3 | AAZ74330 | Downstrea  | 383 | 13.2 | 45.5 | 27 | 4 | AD21655  | Aad21655  | SV40 prom |
| 311 | 13.2 | 45.5 | 27 | 3 | AAZ87659 | Downstrea  | 384 | 13.2 | 45.5 | 27 | 4 | AAZ91287 | Aac91287  | SV40 prom |
| 312 | 13.2 | 45.5 | 27 | 3 | AAZ98994 | SV40 earl  | 385 | 13.2 | 45.5 | 27 | 4 | AAZ72342 | Aaf72342  | Downstrea |
| 313 | 13.2 | 45.5 | 27 | 3 | AAC81021 | Downstrea  | 386 | 13.2 | 45.5 | 27 | 4 | AAZ62746 | Aaf62746  | 3' primer |
| 314 | 13.2 | 45.5 | 27 | 3 | AAC55183 | Downstrea  | 387 | 13.2 | 45.5 | 27 | 4 | AAZ37198 | Aah37198  | SV40 prom |
| 315 | 13.2 | 45.5 | 27 | 3 | AAC95455 | Downstrea  | 388 | 13.2 | 45.5 | 27 | 4 | AAZ05572 | Aad05572  | SV40 prom |

|     |      |      |    |   |          |          |           |     |      |      |    |   |           |           |
|-----|------|------|----|---|----------|----------|-----------|-----|------|------|----|---|-----------|-----------|
| 389 | 13.2 | 45.5 | 27 | 4 | AAD08481 | Aad08481 | SV40 prom | 462 | 13.2 | 45.5 | 27 | 5 | AAS29023  | Downstrea |
| 390 | 13.2 | 45.5 | 27 | 4 | AAS08545 | Aas08545 | PCR prime | 463 | 13.2 | 45.5 | 27 | 5 | AAS11940  | SV40 PCR  |
| 391 | 13.2 | 45.5 | 27 | 4 | AAS33045 | Aas33045 | PCR prime | 464 | 13.2 | 45.5 | 27 | 5 | ABK51268  | SV40 prom |
| 392 | 13.2 | 45.5 | 27 | 4 | AAD16575 | Aad16575 | SV40 prom | 465 | 13.2 | 45.5 | 27 | 5 | ABK12723  | Human DNA |
| 393 | 13.2 | 45.5 | 27 | 4 | AAS34760 | Aas34760 | Downstrea | 466 | 13.2 | 45.5 | 27 | 5 | ABAI0997  | Downstrea |
| 394 | 13.2 | 45.5 | 27 | 4 | AAD13297 | Aad13297 | SV40 prom | 467 | 13.2 | 45.5 | 27 | 5 | AAC90331  | Downstrea |
| 395 | 13.2 | 45.5 | 27 | 4 | AAD13291 | Aad13291 | SV40 prom | 468 | 13.2 | 45.5 | 27 | 5 | AAC90337  | Downstrea |
| 396 | 13.2 | 45.5 | 27 | 4 | AAD22304 | Aad22304 | Simian vi | 469 | 13.2 | 45.5 | 27 | 5 | AAF24144  | Downstrea |
| 397 | 13.2 | 45.5 | 27 | 4 | ABAB3187 | Abab3187 | Downstrea | 470 | 13.2 | 45.5 | 27 | 5 | AAS40063  | SV40 prom |
| 398 | 13.2 | 45.5 | 27 | 4 | AAD03477 | Aad03477 | Downstrea | 471 | 13.2 | 45.5 | 27 | 5 | AAD16650  | SV40 prom |
| 399 | 13.2 | 45.5 | 27 | 4 | AAS02633 | Aas02633 | Human sec | 472 | 13.2 | 45.5 | 27 | 5 | AAS12127  | Human lun |
| 400 | 13.2 | 45.5 | 27 | 4 | AH31342  | Aah31342 | SV40 prom | 473 | 13.2 | 45.5 | 27 | 5 | AAH46848  | GAS-SV40  |
| 401 | 13.2 | 45.5 | 27 | 4 | AAF63782 | Aaf63782 | Downstrea | 474 | 13.2 | 45.5 | 27 | 5 | AAS00859  | SV40 PCR  |
| 402 | 13.2 | 45.5 | 27 | 4 | AAD07564 | Aad07564 | SV40 prom | 475 | 13.2 | 45.5 | 27 | 5 | Aaf85178  | PCR prime |
| 403 | 13.2 | 45.5 | 27 | 4 | AAS02515 | Aah32515 | SV40 prom | 476 | 13.2 | 45.5 | 27 | 5 | AAD05382  | SV40 prom |
| 404 | 13.2 | 45.5 | 27 | 4 | AAH19163 | Aah19163 | SV40 prom | 477 | 13.2 | 45.5 | 27 | 5 | AAD07648  | SV40 prom |
| 405 | 13.2 | 45.5 | 27 | 4 | AAI19541 | Aai19541 | Downstrea | 478 | 13.2 | 45.5 | 27 | 5 | AAS12078  | Human TNF |
| 406 | 13.2 | 45.5 | 27 | 4 | AAH48338 | Aah48338 | SV40 earl | 479 | 13.2 | 45.5 | 27 | 5 | AAH46926  | GAS-SV40  |
| 407 | 13.2 | 45.5 | 27 | 4 | AAD08397 | Aad08397 | SV40 prom | 480 | 13.2 | 45.5 | 27 | 5 | AAC91277  | SV40 prom |
| 408 | 13.2 | 45.5 | 27 | 4 | AAF33088 | Aaf33088 | Downstrea | 481 | 13.2 | 45.5 | 27 | 5 | AAC90699  | SV40 prom |
| 409 | 13.2 | 45.5 | 27 | 4 | AAS03875 | Aas03875 | Human sec | 482 | 13.2 | 45.5 | 27 | 5 | AAC90699  | SV40 prom |
| 410 | 13.2 | 45.5 | 27 | 4 | AAD07763 | Aad07763 | SV40 prom | 483 | 13.2 | 45.5 | 27 | 5 | AAD07698  | SV40 prom |
| 411 | 13.2 | 45.5 | 27 | 4 | AAD05485 | Aad05485 | SV40 prom | 484 | 13.2 | 45.5 | 27 | 5 | AAS12109  | Human end |
| 412 | 13.2 | 45.5 | 27 | 4 | AAD04891 | Aad04891 | SV40 prom | 485 | 13.2 | 45.5 | 27 | 5 | AAS121714 | Human liv |
| 413 | 13.2 | 45.5 | 27 | 4 | AAD08184 | Aad08184 | SV40 prom | 486 | 13.2 | 45.5 | 27 | 5 | AAS139341 | Downstrea |
| 414 | 13.2 | 45.5 | 27 | 4 | AAS28876 | Aas28876 | Human imm | 487 | 13.2 | 45.5 | 27 | 5 | AAS12668  | SV40 PCR  |
| 415 | 13.2 | 45.5 | 27 | 4 | AAS12063 | Aas12063 | Human imm | 488 | 13.2 | 45.5 | 27 | 6 | ABK51862  | Downstrea |
| 416 | 13.2 | 45.5 | 27 | 4 | AAS28877 | Aas28877 | Human imm | 489 | 13.2 | 45.5 | 27 | 6 | ABK51862  | Downstrea |
| 417 | 13.2 | 45.5 | 27 | 4 | AAS11962 | Aas11962 | SV40 PCR  | 490 | 13.2 | 45.5 | 27 | 6 | AD44629   | SV40 prom |
| 418 | 13.2 | 45.5 | 27 | 4 | AAK54944 | Aak54944 | Downstrea | 491 | 13.2 | 45.5 | 27 | 6 | AD44629   | SV40 prom |
| 419 | 13.2 | 45.5 | 27 | 4 | ABK11281 | Abk11281 | SV40 prom | 492 | 13.2 | 45.5 | 27 | 6 | AD44629   | SV40 prom |



|       |      |      |    |   |          |                     |       |      |      |    |    |          |                     |
|-------|------|------|----|---|----------|---------------------|-------|------|------|----|----|----------|---------------------|
| 681   | 13   | 44.8 | 25 | 6 | ABQ12786 | Abq12786 Oligonucle | C 754 | 12.8 | 44.1 | 26 | 2  | AAZ25364 | Aaz25364 Rat        |
| 682   | 13   | 44.8 | 25 | 8 | ACI30448 | ACI30448 Human mic  | C 755 | 12.8 | 44.1 | 26 | 4  | AAZ10865 | Aaz10865 Rat        |
| 683   | 13   | 44.8 | 25 | 3 | ABK50422 | ABK50422 Human tra  | C 756 | 12.8 | 44.1 | 27 | 3  | AAA08419 | Aaa08419 Human cum  |
| C 684 | 13   | 44.8 | 33 | 6 | ABL54251 | ABL54251 Human nuc  | C 757 | 12.8 | 44.1 | 30 | 6  | ABX67974 | Abx67974 Novel Hel  |
| C 685 | 13   | 44.8 | 38 | 4 | ABK05323 | ABK05323 Human NOG  | C 758 | 12.8 | 44.1 | 30 | 6  | ABX69591 | Abx69591 Novel Hel  |
| C 686 | 13   | 44.8 | 44 | 9 | ADC17368 | ADC17368 3' primer  | C 759 | 12.8 | 44.1 | 31 | 2  | AAX39384 | Aax39384 Human gen  |
| C 687 | 13   | 44.8 | 48 | 3 | AAZ47019 | AAZ47019 Primer JC  | C 760 | 12.8 | 44.1 | 31 | 2  | AAX39231 | Aax39231 Human gen  |
| C 688 | 13   | 44.8 | 48 | 6 | ABN72174 | ABN72174 Streptoco  | C 761 | 12.8 | 44.1 | 31 | 4  | ABK06479 | Abk06479 Human NOG  |
| C 689 | 13   | 44.8 | 49 | 2 | AAV20409 | AAV20409 Human eer  | C 762 | 12.8 | 44.1 | 31 | 4  | ABK21754 | Abk21754 Human ERG  |
| C 690 | 13   | 44.8 | 49 | 6 | ABN52984 | ABN52984 Human IGE  | C 763 | 12.8 | 44.1 | 31 | 7  | ACA08645 | Aca08645 Necroel    |
| C 691 | 13   | 44.8 | 50 | 4 | AAI30837 | AAI30837 Human SNP  | C 764 | 12.8 | 44.1 | 31 | 7  | ABA05933 | Abao5933 Human K-R  |
| C 692 | 13   | 44.8 | 50 | 4 | AAI31756 | AAI31756 Human SNP  | C 765 | 12.8 | 44.1 | 32 | 6  | ABA05933 | Abao5933 Human ubi  |
| C 693 | 13   | 44.8 | 50 | 6 | ABZ07660 | ABZ07660 Human leu  | C 766 | 12.8 | 44.1 | 39 | 7  | ABX99212 | Abx99212 Human CAN  |
| C 694 | 13   | 44.8 | 50 | 6 | ABZ05329 | ABZ05329 Human clo  | C 767 | 12.8 | 44.1 | 41 | 6  | ABZ48772 | Abz48772 Human ald  |
| C 695 | 13   | 44.8 | 51 | 3 | AAZ77092 | AAZ77092 Human SNP  | C 768 | 12.8 | 44.1 | 41 | 6  | ABZ46261 | Abz46261 Human ald  |
| C 696 | 13   | 44.8 | 51 | 4 | AAI29046 | AAI29046 Human SNP  | C 769 | 12.8 | 44.1 | 42 | 2  | AAQ36455 | Aaq36455 Mutagenic  |
| C 697 | 13   | 44.8 | 51 | 4 | AAI28235 | AAI28235 Human SNP  | C 770 | 12.8 | 44.1 | 45 | 2  | AAQ69592 | Aaq69592 Human gen  |
| C 698 | 13   | 44.8 | 51 | 4 | AAI74331 | AAI74331 Human sil  | C 771 | 12.8 | 44.1 | 45 | 2  | AAQ69380 | Aaq69380 Human fib  |
| C 699 | 13   | 44.8 | 51 | 4 | AAH38768 | AAH38768 Human SNP  | C 772 | 12.8 | 44.1 | 45 | 2  | AAT64054 | Aat64054 Human fib  |
| C 700 | 13   | 44.8 | 51 | 8 | ADA94847 | ADA94847 Primer P0  | C 773 | 12.8 | 44.1 | 45 | 2  | AAT63842 | Aat63842 Human fib  |
| C 701 | 13   | 44.8 | 53 | 2 | AAZ47169 | AAZ47169 Primer JC  | C 774 | 12.8 | 44.1 | 45 | 2  | AAI17130 | Aai17130 Test sequ  |
| C 702 | 13   | 44.8 | 54 | 3 | AAZ73969 | AAZ73969 GFP Tyr(T  | C 775 | 12.8 | 44.1 | 45 | 2  | AAI17342 | Aai17342 Test sequ  |
| C 703 | 13   | 44.8 | 54 | 6 | ABQ94682 | ABQ94682 Tumour su  | C 776 | 12.8 | 44.1 | 45 | 6  | ABK82833 | Abk82833 DNA bindi  |
| C 704 | 13   | 44.8 | 55 | 2 | AAQ29522 | AAQ29522 Antisense  | C 777 | 12.8 | 44.1 | 45 | 6  | ABK82621 | Abk82621 DNA bindi  |
| C 705 | 13   | 44.8 | 60 | 6 | ABT12018 | ABT12018 E coli ex  | C 778 | 12.8 | 44.1 | 45 | 10 | ADH80160 | Adh80160 Duplex ol  |
| C 706 | 13   | 44.8 | 60 | 6 | ABN46823 | ABN46823 Human spl  | C 779 | 12.8 | 44.1 | 45 | 10 | ADH80372 | Adh80372 Duplex ol  |
| C 707 | 13   | 44.8 | 60 | 6 | ABN45568 | ABN45568 Human spl  | C 780 | 12.8 | 44.1 | 47 | 3  | AAZ66068 | Aaz66068 Human map  |
| C 708 | 13   | 44.8 | 60 | 6 | ABN36148 | ABN36148 Human spl  | C 781 | 12.8 | 44.1 | 48 | 9  | ADD01530 | Add01530 Human del  |
| C 709 | 13   | 44.8 | 60 | 6 | ABN45697 | ABN45697 Human spl  | C 782 | 12.8 | 44.1 | 50 | 2  | AAQ69593 | Aaq69593 Human gen  |
| C 710 | 13   | 44.8 | 65 | 6 | ABZ28160 | ABZ28160 Candida g  | C 783 | 12.8 | 44.1 | 50 | 2  | AAT64055 | Aat64055 Human fib  |
| C 711 | 13   | 44.8 | 65 | 6 | ABZ26554 | ABZ26554 Candida e  | C 784 | 12.8 | 44.1 | 50 | 2  | AAI17343 | Aai17343 Test sequ  |
| C 712 | 13   | 44.8 | 65 | 6 | ABZ26331 | ABZ26331 Candida e  | C 785 | 12.8 | 44.1 | 50 | 4  | AAI29124 | Aai29124 Human SNP  |
| C 713 | 13   | 44.8 | 65 | 6 | ABZ29792 | ABZ29792 Candida g  | C 786 | 12.8 | 44.1 | 50 | 6  | ABK82834 | Abk82834 DNA bindi  |
| C 714 | 13   | 44.8 | 65 | 6 | ABN55646 | ABN55646 Mouse spl  | C 787 | 12.8 | 44.1 | 50 | 6  | ABZ00746 | Abz00746 Human leu  |
| C 715 | 13   | 44.8 | 65 | 6 | ABN29149 | ABN29149 Rat spl    | C 788 | 12.8 | 44.1 | 50 | 10 | ADH80373 | Adh80373 Duplex ol  |
| C 716 | 13   | 44.8 | 65 | 6 | ABN57549 | ABN57549 Mouse spl  | C 789 | 12.8 | 44.1 | 51 | 4  | AAI27909 | Aai27909 Human SNP  |
| C 717 | 13   | 44.8 | 65 | 6 | ABN55388 | ABN55388 Mouse spl  | C 790 | 12.8 | 44.1 | 54 | 3  | AAZ38935 | Aaz38935 hCAT1 bin  |
| C 718 | 13   | 44.8 | 65 | 6 | ABN56758 | ABN56758 Mouse spl  | C 791 | 12.8 | 44.1 | 54 | 3  | AAZ38741 | Aaz38741 hCAT1 bin  |
| C 719 | 13   | 44.8 | 65 | 6 | ABN55469 | ABN55469 Mouse spl  | C 792 | 12.8 | 44.1 | 57 | 3  | AAA65212 | Aaa65212 Savinase   |
| C 720 | 13   | 44.8 | 65 | 6 | ABN57539 | ABN57539 Mouse spl  | C 793 | 12.8 | 44.1 | 60 | 6  | ABN43416 | Abn43416 Human spl  |
| C 721 | 13   | 44.8 | 66 | 8 | AAI62774 | AAI62774 Escherich  | C 794 | 12.8 | 44.1 | 60 | 6  | ABN33663 | Abn33663 Human spl  |
| C 722 | 13   | 44.8 | 67 | 3 | AAZ70124 | AAZ70124 TGF-beta-  | C 795 | 12.8 | 44.1 | 60 | 6  | ABN44322 | Abn44322 Human spl  |
| C 723 | 13   | 44.8 | 70 | 5 | AAZ29228 | AAZ29228 Ligand to  | C 796 | 12.8 | 44.1 | 60 | 6  | ABN48127 | Abn48127 Human spl  |
| C 724 | 13   | 44.8 | 72 | 2 | AAQ67708 | AAQ67708 Fragment   | C 797 | 12.8 | 44.1 | 60 | 6  | ABN36863 | Abn36863 Human spl  |
| C 725 | 13   | 44.8 | 72 | 2 | AAQ67331 | AAQ67331 Aait opti  | C 798 | 12.8 | 44.1 | 60 | 6  | ABN47014 | Abn47014 Human spl  |
| C 726 | 13   | 44.8 | 72 | 2 | AAV18224 | AAV18224 Oligomer   | C 799 | 12.8 | 44.1 | 60 | 6  | ABN41377 | Abn41377 Human spl  |
| C 727 | 13   | 44.8 | 72 | 3 | AAZ1624  | AAZ1624 Human sec   | C 800 | 12.8 | 44.1 | 60 | 6  | ABN41672 | Abn41672 Human spl  |
| C 728 | 13   | 44.8 | 73 | 4 | AAZ01051 | AAZ01051 Synthetic  | C 801 | 12.8 | 44.1 | 63 | 2  | AAQ26745 | Aaq26745 VL-PAL fu  |
| C 729 | 13   | 44.8 | 77 | 4 | AAZ01050 | AAZ01050 Synthetic  | C 802 | 12.8 | 44.1 | 63 | 2  | AAQ28095 | Abz28095 Candida g  |
| C 730 | 13   | 44.8 | 77 | 6 | AAZ22494 | AAZ22494 F3R3F1 pr  | C 803 | 12.8 | 44.1 | 65 | 6  | ABZ26220 | Abz26220 Candida e  |
| C 731 | 13   | 44.8 | 77 | 6 | AAZ22495 | AAZ22495 F3R32 pri  | C 804 | 12.8 | 44.1 | 65 | 6  | ABZ26704 | Abz26704 Candida e  |
| C 732 | 13   | 44.8 | 78 | 6 | ABN53536 | ABN53536 Human-mur  | C 805 | 12.8 | 44.1 | 65 | 6  | ABZ26664 | Abz26664 Candida e  |
| C 733 | 13   | 44.8 | 79 | 7 | ACD94842 | ACD94842 Human col  | C 806 | 12.8 | 44.1 | 65 | 6  | ABZ27074 | Abz27074 Candida e  |
| C 734 | 12.8 | 44.1 | 17 | 6 | ABN74758 | ABN74758 Human PAP  | C 807 | 12.8 | 44.1 | 65 | 6  | ABN28506 | Abn28506 Rat spl    |
| C 735 | 12.8 | 44.1 | 17 | 6 | ABN74756 | ABN74756 Human PAP  | C 808 | 12.8 | 44.1 | 65 | 6  | ABN52430 | Abn52430 Mouse spl  |
| C 736 | 12.8 | 44.1 | 18 | 3 | AAZ71110 | AAZ71110 Human bla  | C 809 | 12.8 | 44.1 | 65 | 6  | ABN55121 | Abn55121 Mouse spl  |
| C 737 | 12.8 | 44.1 | 18 | 3 | ABZ71110 | ABZ71110 Human mou  | C 810 | 12.8 | 44.1 | 65 | 6  | ABN55121 | Abn55121 Mouse spl  |
| C 738 | 12.8 | 44.1 | 20 | 7 | ABZ90675 | ABZ90675 Human oli  | C 811 | 12.8 | 44.1 | 65 | 6  | ABN55715 | Abn55715 Staphyloc  |
| C 739 | 12.8 | 44.1 | 20 | 7 | ABZ90675 | ABZ90675 Human oli  | C 812 | 12.8 | 44.1 | 68 | 2  | AAV77073 | Aav77073 Staphyloc  |
| C 740 | 12.8 | 44.1 | 23 | 2 | AAZ33129 | AAZ33129 Treponema  | C 813 | 12.8 | 44.1 | 68 | 3  | AAQ20618 | Aaq20618 Human sec  |
| C 741 | 12.8 | 44.1 | 24 | 2 | AAZ29671 | AAZ29671 PCR Prime  | C 814 | 12.8 | 44.1 | 68 | 3  | AAQ16727 | Aaq16727 Human sec  |
| C 742 | 12.8 | 44.1 | 24 | 3 | AAK99631 | AAK99631 Human S4   | C 815 | 12.8 | 44.1 | 77 | 2  | AAQ62389 | Aaq62389 bioD - bi  |
| C 743 | 12.8 | 44.1 | 25 | 3 | AAK96387 | AAK96387 HLA DPB1   | C 816 | 12.8 | 44.1 | 79 | 2  | AAV64747 | Aav64747 HIV anti-  |
| C 744 | 12.8 | 44.1 | 25 | 6 | ABN03205 | ABN03205 Human GDM  | C 817 | 12.8 | 44.1 | 79 | 7  | ACA74065 | Aca74065 Hepatitis  |
| C 745 | 12.8 | 44.1 | 25 | 6 | ABN03204 | ABN03204 Human GDM  | C 818 | 12.8 | 44.1 | 79 | 7  | ACA74065 | Aca74065 Hepatitis  |
| C 746 | 12.8 | 44.1 | 25 | 6 | ABN97741 | ABN97741 Human NED  | C 819 | 12.6 | 43.4 | 21 | 6  | ABK68014 | Abk68014 Human FCH  |
| C 747 | 12.8 | 44.1 | 25 | 6 | ABN97739 | ABN97739 Human NED  | C 820 | 12.6 | 43.4 | 21 | 6  | ABK70918 | Abk70918 Human fam  |
| C 748 | 12.8 | 44.1 | 25 | 6 | ABN75581 | ABN75581 Human PAP  | C 821 | 12.6 | 43.4 | 21 | 6  | ADAI5057 | Ada15057 Human FCH  |
| C 749 | 12.8 | 44.1 | 25 | 8 | ACK25844 | ACK25844 Human mic  | C 822 | 12.6 | 43.4 | 21 | 8  | ADAI5057 | Ada15057 Human FCH  |
| C 750 | 12.8 | 44.1 | 25 | 8 | ACK25844 | ACK25844 Human mic  | C 823 | 12.6 | 43.4 | 21 | 8  | ADAI5057 | Ada15057 Human FCH  |
| C 751 | 12.8 | 44.1 | 25 | 8 | ACK25844 | ACK25844 Human mic  | C 824 | 12.6 | 43.4 | 22 | 7  | ACF64048 | Acf64048 ESR1 reve  |
| C 752 | 12.8 | 44.1 | 25 | 8 | ACK25844 | ACK25844 Human mic  | C 825 | 12.6 | 43.4 | 22 | 6  | ABQ01430 | Abq01430 Oligonucle |
| C 753 | 12.8 | 44.1 | 25 | 8 | ACK25844 | ACK25844 Human mic  | C 826 | 12.6 | 43.4 | 24 | 6  | ABQ06792 | Abq06792 Oligonucle |

|       |      |      |    |   |           |                     |       |      |      |    |   |           |                     |
|-------|------|------|----|---|-----------|---------------------|-------|------|------|----|---|-----------|---------------------|
| C 827 | 12.6 | 43.4 | 24 | 6 | ABQ66833  | Abq66833 Oligonucle | 900   | 12.6 | 43.4 | 60 | 6 | ABN50311  | Abn50311 Human spl  |
| 828   | 12.6 | 43.4 | 24 | 7 | ABZ70877  | Abz70877 Human mal  | 901   | 12.6 | 43.4 | 60 | 6 | ABN41771  | Abn41771 Human spl  |
| 829   | 12.6 | 43.4 | 25 | 8 | ACI29793  | Act29793 Human mic  | 902   | 12.6 | 43.4 | 60 | 6 | ABN35672  | Abn35672 Human spl  |
| C 830 | 12.6 | 43.4 | 25 | 8 | ACH63509  | Ach63509 DNA targe  | C 903 | 12.6 | 43.4 | 60 | 6 | ABN32296  | Abn32296 Human spl  |
| C 831 | 12.6 | 43.4 | 25 | 8 | ACH63383  | Ach63383 DNA targe  | C 904 | 12.6 | 43.4 | 60 | 6 | ABN42170  | Abn42170 Human spl  |
| 832   | 12.6 | 43.4 | 26 | 2 | AAZ39472  | Aaz39472 A. tumefa  | C 905 | 12.6 | 43.4 | 60 | 9 | AD887528  | Ad887528 Bovine la  |
| 833   | 12.6 | 43.4 | 26 | 4 | AAF93934  | Aaf93934 BAP28 gen  | C 906 | 12.6 | 43.4 | 61 | 7 | ABT21735  | Abt21735 Breast ca  |
| 834   | 12.6 | 43.4 | 26 | 9 | ADC84624  | Adc84624 p33 cloni  | C 907 | 12.6 | 43.4 | 61 | 7 | ABX79947  | Abx79947 EST polym  |
| C 835 | 12.6 | 43.4 | 29 | 2 | AAT51441  | Aat51441 Mouse hea  | C 908 | 12.6 | 43.4 | 64 | 2 | AAT17547  | Aat17547 T. littora |
| C 836 | 12.6 | 43.4 | 29 | 2 | AAQ83497  | Aaq83497 MAB 3B9 g  | C 909 | 12.6 | 43.4 | 65 | 6 | ABZ26491  | Abz26491 Candida e  |
| C 837 | 12.6 | 43.4 | 29 | 2 | AAQ834103 | Aaq834103 Mouse gam | 910   | 12.6 | 43.4 | 65 | 6 | ABZ28150  | Abz28150 Candida g  |
| C 838 | 12.6 | 43.4 | 29 | 2 | AAV03498  | Aav03498 Mouse gam  | C 911 | 12.6 | 43.4 | 65 | 6 | ABZ28341  | Abz28341 Candida g  |
| C 839 | 12.6 | 43.4 | 29 | 2 | AAZ85897  | Aaz85897 Heavy cha  | C 912 | 12.6 | 43.4 | 65 | 6 | ABN30287  | Abn30287 Rat splic  |
| C 840 | 12.6 | 43.4 | 29 | 2 | AAZ28495  | Aaz28495 PCR prime  | 913   | 12.6 | 43.4 | 65 | 6 | ABN31832  | Abn31832 Rat splic  |
| C 841 | 12.6 | 43.4 | 29 | 2 | AAZ79522  | Aaz79522 PCR prime  | 914   | 12.6 | 43.4 | 66 | 6 | ABS52355  | Abs52355 Escherich  |
| C 842 | 12.6 | 43.4 | 30 | 2 | AAT51365  | Aat51365 Marek's d  | 915   | 12.6 | 43.4 | 72 | 1 | AAAN92382 | Aaan92382 Sequence  |
| 843   | 12.6 | 43.4 | 30 | 4 | AAD21464  | Aad21464 O. volvul  | C 916 | 12.6 | 43.4 | 74 | 7 | ABZ70378  | Abz70378 Streptavi  |
| 844   | 12.6 | 43.4 | 30 | 7 | ABZ57988  | Abz57988 Potato si  | C 917 | 12.6 | 43.4 | 75 | 2 | AAQ62654  | Aaq62654 Tobacco-m  |
| C 845 | 12.6 | 43.4 | 31 | 7 | AAV67655  | Aav67655 Nucleotid  | C 918 | 12.6 | 43.4 | 79 | 4 | AAK55455  | Aak55455 Human imm  |
| C 846 | 12.6 | 43.4 | 31 | 7 | ACA08357  | Aca08357 Necrosis   | 919   | 12.6 | 43.4 | 79 | 8 | AAZ57952  | Aaz57952 PCR prime  |
| C 847 | 12.6 | 43.4 | 31 | 7 | ABZ63911  | Abz63911 Human H-R  | C 920 | 12.6 | 43.4 | 80 | 2 | AAT42515  | Aat42515 Sequence   |
| C 848 | 12.6 | 43.4 | 31 | 7 | ABZ63853  | Abz63853 Human H-R  | 921   | 12.6 | 43.4 | 80 | 8 | AAL56764  | Aal56764 Target ol  |
| C 849 | 12.6 | 43.4 | 31 | 7 | ABZ62265  | Abz62265 Human K-R  | 922   | 12.6 | 43.4 | 80 | 8 | AAL52315  | Aal52315 Intercala  |
| C 850 | 12.6 | 43.4 | 31 | 7 | ABZ64179  | Abz64179 Human H-R  | 923   | 12.6 | 43.4 | 80 | 8 | AAL57339  | Aal57339 DNA targ   |
| C 851 | 12.6 | 43.4 | 31 | 7 | ACD54727  | Acd54727 HBV DNaz   | 924   | 12.6 | 43.4 | 80 | 9 | ADE52279  | Ade52279 Target DN  |
| C 852 | 12.6 | 43.4 | 31 | 7 | ACD57411  | Acd57411 HCV DNaz   | 925   | 12.4 | 42.8 | 15 | 3 | AZ64356   | Az64356 Substrate   |
| C 853 | 12.6 | 43.4 | 31 | 7 | ACD61350  | Acd61350 HCV DNaz   | 926   | 12.4 | 42.8 | 15 | 6 | ABX01409  | Abx01409 Hepatitis  |
| C 854 | 12.6 | 43.4 | 31 | 7 | ACD55579  | Acd55579 HCV minus  | 927   | 12.4 | 42.8 | 21 | 2 | AAV38751  | Aav38751 PCR prime  |
| C 855 | 12.6 | 43.4 | 32 | 2 | AAV06226  | Aav06226 Primer us  | 928   | 12.4 | 42.8 | 22 | 2 | AAV99612  | Aav99612 Maize clp  |
| C 856 | 12.6 | 43.4 | 32 | 3 | AAA47264  | Aaa47264 Human lig  | 929   | 12.4 | 42.8 | 23 | 9 | ADE14269  | Ade14269 Optineuri  |
| C 857 | 12.6 | 43.4 | 33 | 5 | AAI68374  | Aai68374 Human lig  | C 930 | 12.4 | 42.8 | 24 | 2 | AAQ48650  | Aaq48650 Control m  |
| C 858 | 12.6 | 43.4 | 33 | 6 | AAK99345  | Aak99345 Human zin  | 931   | 12.4 | 42.8 | 24 | 2 | AAT16074  | Aat16074 Ikaros ge  |
| C 859 | 12.6 | 43.4 | 33 | 6 | ABZ25189  | Abz25189 Peroxidas  | 932   | 12.4 | 42.8 | 24 | 6 | AAL48844  | Aal48844 Murine Ik  |
| C 860 | 12.6 | 43.4 | 34 | 2 | AAZ78755  | Aaz78755 Human RAN  | C 933 | 12.4 | 42.8 | 24 | 7 | ABX89729  | Abx89729 Interleuk  |
| 861   | 12.6 | 43.4 | 34 | 2 | AAZ78758  | Aaz78758 Human RAN  | 934   | 12.4 | 42.8 | 25 | 2 | AQ15426   | Aq15426 Vectorsett  |
| C 862 | 12.6 | 43.4 | 35 | 2 | AAZ96671  | Aaz96671 Forward p  | 935   | 12.4 | 42.8 | 25 | 2 | AAV02010  | Aav02010 Upscream   |
| C 863 | 12.6 | 43.4 | 40 | 7 | ACC59609  | Acc59609 S aureus   | 936   | 12.4 | 42.8 | 25 | 3 | AAZ95839  | Aaz95839 HLA HLA-A  |
| C 864 | 12.6 | 43.4 | 41 | 6 | ABZ43979  | Abz43979 Human glu  | 937   | 12.4 | 42.8 | 25 | 3 | AAZ96690  | Aaz96690 HLA HLA-A  |
| C 865 | 12.6 | 43.4 | 42 | 3 | ABZ49571  | Abz49571 Human glu  | 938   | 12.4 | 42.8 | 25 | 3 | AAZ96188  | Aaz96188 16s rRNA   |
| C 866 | 12.6 | 43.4 | 42 | 3 | AAV11113  | Aav11113 Molecular  | 939   | 12.4 | 42.8 | 25 | 3 | AAZ95870  | Aaz95870 HLA HLA-A  |
| C 867 | 12.6 | 43.4 | 42 | 3 | AAV11118  | Aav11118 Molecular  | 940   | 12.4 | 42.8 | 25 | 3 | AAZ96107  | Aaz96107 16s rRNA   |
| C 868 | 12.6 | 43.4 | 42 | 3 | AAV11126  | Aav11126 Molecular  | 941   | 12.4 | 42.8 | 25 | 3 | AAZ96649  | Aaz96649 HLA HLA-A  |
| C 869 | 12.6 | 43.4 | 42 | 3 | AAZ77595  | Aaz77595 Human PRO  | C 942 | 12.4 | 42.8 | 25 | 6 | ABN97742  | Abn97742 Human NED  |
| C 870 | 12.6 | 43.4 | 43 | 3 | AAZ71108  | Aaz71108 Molecular  | C 943 | 12.4 | 42.8 | 25 | 6 | ABN97743  | Abn97743 Human NED  |
| C 871 | 12.6 | 43.4 | 44 | 2 | AAT42486  | Aat42486 3' primer  | 944   | 12.4 | 42.8 | 25 | 8 | ACI95007  | Act95007 Human mic  |
| C 872 | 12.6 | 43.4 | 45 | 7 | ABV93831  | Abv93831 Bacillus   | 945   | 12.4 | 42.8 | 25 | 8 | ACI54817  | Act54817 Human mic  |
| 873   | 12.6 | 43.4 | 45 | 7 | ABV93527  | Abv93527 Bacillus   | C 946 | 12.4 | 42.8 | 25 | 8 | ACI94781  | Act94781 Human mic  |
| C 874 | 12.6 | 43.4 | 46 | 3 | AAZ71092  | Aaz71092 Molecular  | C 947 | 12.4 | 42.8 | 25 | 8 | ACI42213  | Act42213 Human mic  |
| C 875 | 12.6 | 43.4 | 47 | 3 | AAZ55952  | Aaz55952 Human map  | 948   | 12.4 | 42.8 | 25 | 8 | ACK24015  | Ack24015 Human mic  |
| C 876 | 12.6 | 43.4 | 47 | 3 | AAZ56292  | Aaz56292 Human map  | 949   | 12.4 | 42.8 | 25 | 8 | ACK24015  | Ack24015 Human mic  |
| C 877 | 12.6 | 43.4 | 49 | 6 | ABN17158  | Abn17158 Streptoco  | 950   | 12.4 | 42.8 | 26 | 2 | AAQ50450  | Aaq50450 Bovine MTP |
| C 878 | 12.6 | 43.4 | 50 | 4 | AAZ29203  | Aaz29203 Human SNP  | 951   | 12.4 | 42.8 | 26 | 2 | AAQ50435  | Aaq50435 Human MTP  |
| C 879 | 12.6 | 43.4 | 50 | 4 | AAZ29204  | Aaz29204 Human SNP  | 952   | 12.4 | 42.8 | 26 | 3 | AAZ62089  | Aaz62089 Forward p  |
| C 880 | 12.6 | 43.4 | 50 | 4 | AAZ29345  | Aaz29345 Human SNP  | 953   | 12.4 | 42.8 | 26 | 3 | AAZ62089  | Aaz62089 PCR prime  |
| C 881 | 12.6 | 43.4 | 50 | 5 | ABL00012  | Ab100012 Human sll  | 954   | 12.4 | 42.8 | 27 | 4 | AAZ08148  | Aaz08148 PCR prime  |
| 882   | 12.6 | 43.4 | 50 | 5 | ABL00013  | Ab100013 Human sll  | 955   | 12.4 | 42.8 | 27 | 4 | AAZ20333  | Aaz20333 PCR prime  |
| C 883 | 12.6 | 43.4 | 50 | 6 | ABZ01322  | Abz01322 Human leu  | 956   | 12.4 | 42.8 | 27 | 4 | AAZ27286  | Aaz27286 PCR prime  |
| C 884 | 12.6 | 43.4 | 50 | 6 | ABZ03160  | Abz03160 Human leu  | C 957 | 12.4 | 42.8 | 29 | 2 | AAZ25844  | Aaz25844 Human pol  |
| C 885 | 12.6 | 43.4 | 50 | 6 | ABZ00019  | Abz00019 Human leu  | 958   | 12.4 | 42.8 | 29 | 2 | AAZ76799  | Aaz76799 PCR prime  |
| C 886 | 12.6 | 43.4 | 51 | 4 | AAZ31392  | Aaz31392 Human SNP  | C 959 | 12.4 | 42.8 | 29 | 3 | AAA04490  | Aaa04490 Polymorph  |
| C 887 | 12.6 | 43.4 | 51 | 4 | AAZ31424  | Aaz31424 Human SNP  | C 960 | 12.4 | 42.8 | 31 | 3 | AAZ79079  | Aaz79079 Human gen  |
| C 888 | 12.6 | 43.4 | 51 | 4 | AAZ29619  | Aaz29619 Human SNP  | C 961 | 12.4 | 42.8 | 31 | 7 | AAI30740  | Aai30740 Human sin  |
| C 889 | 12.6 | 43.4 | 51 | 4 | AAZ30782  | Aaz30782 Human SNP  | C 962 | 12.4 | 42.8 | 31 | 7 | ABZ63070  | Abz63070 Human K-R  |
| C 890 | 12.6 | 43.4 | 51 | 4 | AAZ31427  | Aaz31427 Human SNP  | C 963 | 12.4 | 42.8 | 33 | 2 | AAQ74172  | Aaq74172 Mouse poo  |
| C 891 | 12.6 | 43.4 | 51 | 4 | AAZ173982 | Aaz173982 Human sll | 964   | 12.4 | 42.8 | 33 | 4 | AAO05236  | Aao05236 A. fumiga  |
| C 892 | 12.6 | 43.4 | 51 | 4 | AAH90333  | Aah90333 Human c10  | 965   | 12.4 | 42.8 | 33 | 4 | AAAD10345 | Aaad10345 A. fumiga |
| C 893 | 12.6 | 43.4 | 51 | 4 | AAH90334  | Aah90334 Human c10  | C 966 | 12.4 | 42.8 | 33 | 5 | AAH73949  | Aah73949 Human alc  |
| C 894 | 12.6 | 43.4 | 53 | 3 | AAH96241  | Aah96241 PCR prime  | 967   | 12.4 | 42.8 | 33 | 6 | AAI73030  | Aai73030 RNA encod  |
| C 895 | 12.6 | 43.4 | 53 | 7 | ADA48841  | Ada48841 PCR prime  | 968   | 12.4 | 42.8 | 33 | 6 | AAI73029  | Aai73029 cDNAenco   |
| C 896 | 12.6 | 43.4 | 54 | 8 | ADA36991  | Ada36991 Mouse H1   | C 969 | 12.4 | 42.8 | 35 | 4 | AAF63484  | Aaf63484 Oligonucle |
| C 897 | 12.6 | 43.4 | 55 | 5 | AAF60029  | Aaf60029 Modified   | C 970 | 12.4 | 42.8 | 36 | 2 | AAT85337  | Aat85337 Spider si  |
| C 898 | 12.6 | 43.4 | 59 | 9 | ADB87653  | Adb87653 S. aureus  | C 971 | 12.4 | 42.8 | 37 | 3 | AAZ92415  | Aaz92415 Plasmid p  |
| 899   | 12.6 | 43.4 | 60 | 6 | ABN41722  | Abn41722 Human spl  | 972   | 12.4 | 42.8 | 38 | 3 | AAZ73295  | Aaz73295 Single ba  |

c 973 12.4 42.8 38 4 ABK08054  
 974 12.4 42.8 38 5 AAD11417 S. cerevisiae  
 975 12.4 42.8 39 3 AAD40165 H. pylori  
 976 12.4 42.8 39 4 AAD09244 A. fumigata  
 977 12.4 42.8 39 4 AAF88116 H. pylori  
 978 12.4 42.8 39 4 AAF88059 H. pylori  
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 981 12.4 42.8 39 6 AAI73042 RNA encod  
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 989 12.4 42.8 41 6 AB247644 Human ATP  
 990 12.4 42.8 41 6 ABK89452 Human kin  
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 995 12.4 42.8 43 6 AB227741 Candida e  
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 998 12.4 42.8 45 4 AAD10349 A. fumigata  
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## ALIGNMENTS

RESULT 1  
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 ID AAA70828 standard; RNA; 29 BP.  
 AC AAA70828;  
 DT 27-APR-2001 (first entry)  
 DE Molecular interaction site RNA #28.  
 KW Modulator; identification; molecular interaction; virtual library; ss.  
 OS Homo sapiens.  
 PN WO9958947-A2.  
 PD 18-NOV-1999.  
 PF 12-MAY-1999; 99WO-US010361.  
 PR 12-MAY-1998; 98US-00076404.  
 PR 12-MAY-1998; 98US-0085092P.  
 PA (ISIS-) ISIS PHARM INC.  
 PI Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;  
 PI Hofstadler S, McNeil J;  
 DR WPI; 2000-086439/07.  
 PT Identifying compounds which modulate activity of target biomolecules,  
 PT used to provide compounds which can be used as pharmacological,  
 PT agricultural and industrial compounds.  
 PS Claim 235; Page 235; 405pp; English.  
 CC This invention describes a novel method for identifying compounds which  
 CC modulate the activity of a target biomolecule. The method uses 3-  
 CC dimensional representations of the biomolecule and a library of compounds  
 CC and comprises (a) identifying at least one molecular interaction site of  
 CC the target RNA; (b) generating in silico a virtual library of compounds

the target RNA; (b) generating in silico a virtual library of compounds  
 predicted or calculated to interact with the molecular interaction site;  
 and (c) comparing 3-dimensional (3-D) representations of the target RNA  
 with members of the virtual library of compounds to generate a hierarchy  
 of the compounds ranked in accordance with their respective ability to  
 form physical interactions with the molecular interaction site. The  
 method also describes (1) RNA comprising a joined sequence of at least 24  
 nucleotides but not more than 70 nucleotides and having secondary  
 structure defined by: (a) 3 nucleotides forming a first side of a first  
 double stranded (ds) region; (b) 2 nucleotides forming a first side of a second  
 internal loop region; (c) 4 nucleotides forming a first side of a second  
 ds region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4  
 nucleotides forming a second side of the second ds region; (f) 4  
 nucleotides forming a second side of the internal loop region; and (g) 3  
 nucleotides forming a second side of the first ds region; (2) a purified  
 and isolated RNA fragment comprising the human sequence  
 UUUACACAAUUCUAGUUUACAGAAAAUUC (II). The methods and products can be  
 used for identifying agents which modulate the activity of biomolecules,  
 particularly RNA. Such agents can be used as pharmaceutical, agricultural  
 or industrial compounds  
 Sequence 29 BP; 5 A; 5 C; 7 G; 0 T; 12 U; 0 Other;  
 Query Match 100.0%; Score 29; DB 3; Length 29;  
 Best Local Similarity 100.0%; Pred No. 0.0026;  
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 UAUAUUCUUUUUGUUAAGCCUAGGGGCU 29  
 |||||  
 DB 1 UAUAUUCUUUUUGUUAAGCCUAGGGGCU 29

RESULT 2  
 AAA71123  
 ID AAA71123 standard; DNA; 42 BP.  
 AC AAA71123;  
 DT 27-APR-2001 (first entry)  
 DE Molecular interaction site DNA #129.  
 KW Modulator; identification; molecular interaction; virtual library; ss.  
 OS Unidentified.  
 PN WO9958947-A2.  
 PD 18-NOV-1999.  
 PF 12-MAY-1999; 99WO-US010361.  
 PR 12-MAY-1998; 98US-00076404.  
 PR 12-MAY-1998; 98US-0085092P.  
 PA (ISIS-) ISIS PHARM INC.  
 PI Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;  
 PI Hofstadler S, McNeil J;  
 DR WPI; 2000-086439/07.  
 PT Identifying compounds which modulate activity of target biomolecules,  
 PT used to provide compounds which can be used as pharmacological,  
 PT agricultural and industrial compounds.  
 PS Example 7; Fig 125; 405pp; English.  
 CC This invention describes a novel method for identifying compounds which  
 CC modulate the activity of a target biomolecule. The method uses 3-  
 CC dimensional representations of the biomolecule and a library of compounds  
 CC and comprises (a) identifying at least one molecular interaction site of  
 CC the target RNA; (b) generating in silico a virtual library of compounds



CC predicted or calculated to interact with the molecular interaction site;  
 CC and (c) comparing 3-dimensional (3-D) representations of the target RNA  
 CC with members of the virtual library of compounds to generate a hierarchy  
 CC of the compounds ranked in accordance with their respective ability to  
 CC form physical interactions with the molecular interaction site. The  
 CC method also describes (1) RNA comprising a joined sequence of at least 24  
 CC nucleotides but not more than 70 nucleotides and having secondary  
 CC structure defined by: (a) 3 nucleotides forming a first side of a first  
 CC double stranded (ds) region; (b) 2 nucleotides forming a first side of an  
 CC internal loop region; (c) 4 nucleotides forming a first side of a second  
 CC ds region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4  
 CC nucleotides forming a second side of the second ds region; and (g) 3  
 CC nucleotides forming a second side of the internal loop region; and (g) 3  
 CC nucleotides forming a second side of the first ds region; (2) a purified  
 CC and isolated RNA fragment comprising the human sequence  
 CC UUUACACAUUAUUGUUAAGCCUAGGGGCU (II). The methods and products can be  
 CC used for identifying agents which modulate the activity of biomolecules,  
 CC particularly RNA. Such agents can be used as pharmaceutical, agricultural  
 CC or industrial compounds  
 XX  
 SQ Sequence 42 BP; 9 A; 6 C; 9 G; 18 T; 0 U; 0 Other;

Query Match 100.0%; Score 29; DB 3; Length 42;  
 Best Local Similarity 58.6%; Pred. No. 0.0027;  
 Matches 17; Conservative 12; Mismatches 0; Indels 0; Gaps 0;

QY 1 UAUGAUUCUUUUUGUUAAGCCUAGGGGCU 29  
 |||||:|||||:|||||:|||||:  
 Db 4 TATGATCTTTTGTAAAGCCCTAGGGGCT 32

RESULT 3  
 AAA71131  
 ID AAA71131 standard; RNA; 42 BP.  
 XX  
 AC AAA71131;  
 XX  
 DT 27-APR-2001 (first entry)  
 DE Molecular interaction site RNA #200.  
 XX  
 KW Modulator; identification; molecular interaction; virtual library; ss.  
 XX  
 OS Unidentified.  
 XX  
 PN W09558947-A2.  
 XX  
 PD 18-NOV-1999.  
 XX  
 PF 12-MAY-1999; 99WO-US010361.  
 XX  
 PR 12-MAY-1998; 98US-00076404.  
 PR 12-MAY-1998; 98US-0085092P.  
 XX  
 PA (ISIS-) ISIS PHARM INC.  
 XX  
 PI Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;  
 PI Hofstadler S, Mcneil J;  
 XX  
 DR WPI; 2000-086439/07.  
 XX

PT Identifying compounds which modulate activity of target biomolecules,  
 PT used to provide compounds which can be used as pharmacological,  
 PT agricultural and industrial compounds.  
 XX  
 PS Example 7; Fig 126; 405pp; English.  
 XX  
 CC This invention describes a novel method for identifying compounds which  
 CC modulate the activity of a target biomolecule. The method uses 3-  
 CC dimensional representations of the biomolecule and a library of compounds  
 CC and comprises (a) identifying at least one molecular interaction site of  
 CC the target RNA; (b) generating in silico a virtual library of compounds  
 CC predicted or calculated to interact with the molecular interaction site;  
 CC

CC and (c) comparing 3-dimensional (3-D) representations of the target RNA  
 CC with members of the virtual library of compounds to generate a hierarchy  
 CC of the compounds ranked in accordance with their respective ability to  
 CC form physical interactions with the molecular interaction site. The  
 CC method also describes (1) RNA comprising a joined sequence of at least 24  
 CC nucleotides but not more than 70 nucleotides and having secondary  
 CC structure defined by: (a) 3 nucleotides forming a first side of a first  
 CC double stranded (ds) region; (b) 2 nucleotides forming a first side of an  
 CC internal loop region; (c) 4 nucleotides forming a first side of a second  
 CC ds region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4  
 CC nucleotides forming a second side of the second ds region; and (g) 3  
 CC nucleotides forming a second side of the internal loop region; and (g) 3  
 CC nucleotides forming a second side of the first ds region; (2) a purified  
 CC and isolated RNA fragment comprising the human sequence  
 CC UUUACACAUUAUUGUUAAGCCUAGGGGCU (II). The methods and products can be  
 CC used for identifying agents which modulate the activity of biomolecules,  
 CC particularly RNA. Such agents can be used as pharmaceutical, agricultural  
 CC or industrial compounds  
 XX  
 SQ Sequence 42 BP; 9 A; 6 C; 9 G; 18 T; 0 U; 0 Other;

Query Match 100.0%; Score 29; DB 3; Length 42;  
 Best Local Similarity 100.0%; Pred. No. 0.0027;  
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 UAUGAUUCUUUUUGUUAAGCCUAGGGGCU 29  
 |||||:|||||:|||||:|||||:  
 Db 4 UAUGAUUCUUUUUGUUAAGCCUAGGGGCU 32

RESULT 4  
 AAA70824  
 ID AAA70824 standard; RNA; 45 BP.  
 XX  
 AC AAA70824;  
 XX  
 DT 27-APR-2001 (first entry)  
 DE Molecular interaction site RNA #24.  
 XX  
 KW Modulator; identification; molecular interaction; virtual library; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W09558947-A2.  
 XX  
 PD 18-NOV-1999.  
 XX  
 PF 12-MAY-1999; 99WO-US010361.  
 XX  
 PR 12-MAY-1998; 98US-00076404.  
 PR 12-MAY-1998; 98US-0085092P.  
 XX  
 PA (ISIS-) ISIS PHARM INC.  
 XX  
 PI Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;  
 PI Hofstadler S, Mcneil J;  
 XX  
 DR WPI; 2000-086439/07.  
 XX

PT Identifying compounds which modulate activity of target biomolecules,  
 PT used to provide compounds which can be used as pharmacological,  
 PT agricultural and industrial compounds.  
 XX  
 PS Claim 220; Page 232; 405pp; English.  
 XX  
 CC This invention describes a novel method for identifying compounds which  
 CC modulate the activity of a target biomolecule. The method uses 3-  
 CC dimensional representations of the biomolecule and a library of compounds  
 CC and comprises (a) identifying at least one molecular interaction site of  
 CC the target RNA; (b) generating in silico a virtual library of compounds  
 CC predicted or calculated to interact with the molecular interaction site;  
 CC and (c) comparing 3-dimensional (3-D) representations of the target RNA  
 CC

CC with members of the virtual library of compounds to generate a hierarchy  
CC of the compounds ranked in accordance with their respective ability to  
CC form physical interactions with the molecular interaction site. The  
CC method also describes (1) RNA comprising a joined sequence of at least 24  
CC nucleotides but not more than 70 nucleotides and having secondary  
CC structure defined by: (a) 3 nucleotides forming a first side of a first  
CC double stranded (ds) region; (b) 2 nucleotides forming a first side of an  
CC internal loop region; (c) 4 nucleotides forming a first side of a second  
CC internal loop region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4  
CC ds region; (f) 4 or 5 nucleotides forming a second side of the second ds region; (g) 3  
CC nucleotides forming a second side of the internal loop region; and (h) 3  
CC nucleotides forming a second side of the first ds region; (2) a purified  
CC and isolated RNA fragment comprising the human sequence  
CC UUUACACAAUUAUCUUAUACAGAAAUAUC (II). The methods and products can be  
CC used for identifying agents which modulate the activity of biomolecules,  
CC particularly RNA. Such agents can be used as pharmaceutical, agricultural  
CC or industrial compounds  
XX  
SQ Sequence 45 BP; 11 A; 6 C; 9 G; 0 T; 19 U; 0 Other;

Query Match 96.6%; Score 28; DB 3; Length 45;  
Best Local Similarity 100.0%; Pred. No. 0.0077;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 UAUUAUUUUUUUUUAAGCCUAGGGGC 28  
18 UAUUAUUUUUUUUUAAGCCUAGGGGC 45  
DB

RESULT 5  
AAA71087  
ID AAA71087 standard; DNA; 46 BP.  
AC  
XX AAA71087;  
XX  
DT 27-APR-2001 (first entry)  
XX  
DE Molecular interaction site DNA #110.  
KW Modulator; identification; molecular interaction; virtual library; ss.

OS Unidentified.  
XX WO9958947-A2.  
XX 18-NOV-1999.  
XX  
PF 12-MAY-1999; 99WO-US010361.  
XX  
PR 12-MAY-1998; 98US-00076404.  
PR 12-MAY-1998; 98US-0085092P.  
XX (ISIS-) ISIS PHARM INC.  
XX  
XX Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;  
PI Hofstadler S, McNeil J;  
XX  
XX WPI; 2000-086439/07.  
XX

Identifying compounds which modulate activity of target biomolecules,  
PT used to provide compounds which can be used as pharmacological,  
PT agricultural and industrial compounds.

XX Example 7; Fig 121; 405pp; English.

XX This invention describes a novel method for identifying compounds which  
CC modulate the activity of a target biomolecule. The method uses 3-  
CC dimensional representations of the biomolecule and a library of compounds  
CC and comprises (a) identifying at least one molecular interaction site of  
CC the target RNA; (b) generating in silico a virtual library of compounds  
CC predicted or calculated to interact with the molecular interaction site;  
CC and (c) comparing 3-dimensional (3-D) representations of the target RNA  
CC with members of the virtual library of compounds to generate a hierarchy

CC of the compounds ranked in accordance with their respective ability to  
CC form physical interactions with the molecular interaction site. The  
CC method also describes (1) RNA comprising a joined sequence of at least 24  
CC nucleotides but not more than 70 nucleotides and having secondary  
CC structure defined by: (a) 3 nucleotides forming a first side of a first  
CC double stranded (ds) region; (b) 2 nucleotides forming a first side of an  
CC internal loop region; (c) 4 nucleotides forming a first side of a second  
CC internal loop region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4  
CC ds region; (f) 4 or 5 nucleotides forming a second side of the second ds region; (g) 3  
CC nucleotides forming a second side of the internal loop region; and (h) 3  
CC nucleotides forming a second side of the first ds region; (2) a purified  
CC and isolated RNA fragment comprising the human sequence  
CC UUUACACAAUUAUCUUAUACAGAAAUAUC (II). The methods and products can be  
CC used for identifying agents which modulate the activity of biomolecules,  
CC particularly RNA. Such agents can be used as pharmaceutical, agricultural  
CC or industrial compounds  
XX  
SQ Sequence 46 BP; 11 A; 7 C; 9 G; 19 T; 0 U; 0 Other;

Query Match 96.6%; Score 28; DB 3; Length 46;  
Best Local Similarity 60.7%; Pred. No. 0.0077;  
Matches 17; Conservative 11; Mismatches 0; Indels 0; Gaps 0;  
QY 1 UAUUAUUUUUUUUUAAGCCUAGGGGC 28  
19 TATGATCTTTTGTAAAGCCCTAGGGGC 46  
DB

RESULT 6  
AAA71096  
ID AAA71096 standard; DNA; 46 BP.  
AC  
XX AAA71096;  
XX  
DT 27-APR-2001 (first entry)  
XX  
DE Molecular interaction site DNA #119.  
KW Modulator; identification; molecular interaction; virtual library; ss.

OS Unidentified.  
XX WO9958947-A2.  
XX 18-NOV-1999.  
XX  
PF 12-MAY-1999; 99WO-US010361.  
XX  
PR 12-MAY-1998; 98US-00076404.  
PR 12-MAY-1998; 98US-0085092P.  
XX (ISIS-) ISIS PHARM INC.  
XX  
XX Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;  
PI Hofstadler S, McNeil J;  
XX  
XX WPI; 2000-086439/07.  
XX

Identifying compounds which modulate activity of target biomolecules,  
PT used to provide compounds which can be used as pharmacological,  
PT agricultural and industrial compounds.

XX Example 7; Fig 121; 405pp; English.

XX This invention describes a novel method for identifying compounds which  
CC modulate the activity of a target biomolecule. The method uses 3-  
CC dimensional representations of the biomolecule and a library of compounds  
CC and comprises (a) identifying at least one molecular interaction site of  
CC the target RNA; (b) generating in silico a virtual library of compounds  
CC predicted or calculated to interact with the molecular interaction site;  
CC and (c) comparing 3-dimensional (3-D) representations of the target RNA  
CC with members of the virtual library of compounds to generate a hierarchy  
CC of the compounds ranked in accordance with their respective ability to

CC form physical interactions with the molecular interaction site. The  
 CC method also describes (1) RNA comprising a joined sequence of at least 24  
 CC nucleotides but not more than 70 nucleotides and having secondary  
 CC structure defined by: (a) 3 nucleotides forming a first side of a first  
 CC double stranded (ds) region; (b) 2 nucleotides forming a first side of an  
 CC internal loop region; (c) 4 nucleotides forming a first side of a second  
 CC ds region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4  
 CC nucleotides forming a second side of the second ds region; (f) 4  
 CC nucleotides forming a second side of the internal loop region; and (g) 3  
 CC nucleotides forming a second side of the first ds region; (2) a purified  
 CC and isolated RNA fragment comprising the human sequence  
 CC UUUACACAAUUCUAGUUUACAGAAAUC (II). The methods and products can be  
 CC used for identifying agents which modulate the activity of biomolecules,  
 CC particularly RNA. Such agents can be used as pharmaceutical, agricultural  
 CC or industrial compounds

XX Sequence 46 BP; 11 A; 7 C; 9 G; 19 T; 0 U; 0 Other;  
 SQ

Query Match 96.6%; Score 28; DB 3; Length 46;  
 Best Local Similarity 60.7%; Pred. No. 0.0077;  
 Matches 17; Conservative 11; Mismatches 0; Indels 0; Gaps 0;

QY 1 UAUAGUUCUUUUUUAAGCCUAGGGC 28  
 Db 19 TATGATCTTTTGTAAAGCCCTAGGGC 46

RESULT 7  
 AAA71099  
 ID AAA71099 standard; DNA; 46 BP.  
 XX  
 AC AAA71099;  
 XX  
 DT 27-APR-2001 (first entry)  
 XX  
 DE Molecular interaction site DNA #122.  
 XX  
 KW Modulator; identification; molecular interaction; virtual library; ss.

XX Unidentified.  
 OS  
 XX WO9958947-A2.  
 PN  
 XX 18-NOV-1999.  
 PD  
 XX 12-MAY-1999; 99WO-US010361.  
 PF  
 XX 12-MAY-1998; 98US-00076404.  
 PR  
 XX 12-MAY-1998; 98US-0085092P.  
 XX  
 PA (ISIS-) ISIS PHARM INC.  
 XX  
 XX Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;  
 PI Hofstadler S, Mcneil J;  
 XX  
 DR WPI; 2000-086439/07.  
 XX  
 XX Identifying compounds which modulate activity of target biomolecules,  
 PT used to provide compounds which can be used as pharmacological,  
 PT agricultural and industrial compounds.  
 XX  
 XX Example 7; Fig 121; 405pp; English.

XX This invention describes a novel method for identifying compounds which  
 CC modulate the activity of a target biomolecule. The method uses 3-  
 CC dimensional representations of the biomolecule and a library of compounds  
 CC and comprises (a) identifying at least one molecular interaction site of  
 CC the target RNA; (b) generating in silico a virtual library of compounds  
 CC predicted or calculated to interact with the molecular interaction site;  
 CC and (c) comparing 3-dimensional (3-D) representations of the target RNA  
 CC with members of the virtual library of compounds to generate a hierarchy  
 CC of the compounds ranked in accordance with their respective ability to  
 CC form physical interactions with the molecular interaction site. The

CC method also describes (1) RNA comprising a joined sequence of at least 24  
 CC nucleotides but not more than 70 nucleotides and having secondary  
 CC structure defined by: (a) 3 nucleotides forming a first side of a first  
 CC double stranded (ds) region; (b) 2 nucleotides forming a first side of an  
 CC internal loop region; (c) 4 nucleotides forming a first side of a second  
 CC ds region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4  
 CC nucleotides forming a second side of the second ds region; (f) 4  
 CC nucleotides forming a second side of the internal loop region; and (g) 3  
 CC nucleotides forming a second side of the first ds region; (2) a purified  
 CC and isolated RNA fragment comprising the human sequence  
 CC UUUACACAAUUCUAGUUUACAGAAAUC (II). The methods and products can be  
 CC used for identifying agents which modulate the activity of biomolecules,  
 CC particularly RNA. Such agents can be used as pharmaceutical, agricultural  
 CC or industrial compounds

XX Sequence 46 BP; 11 A; 7 C; 9 G; 19 T; 0 U; 0 Other;

Query Match 96.6%; Score 28; DB 3; Length 46;  
 Best Local Similarity 60.7%; Pred. No. 0.0077;  
 Matches 17; Conservative 11; Mismatches 0; Indels 0; Gaps 0;

QY 1 UAUAGUUCUUUUUUAAGCCUAGGGC 28  
 Db 19 TATGATCTTTTGTAAAGCCCTAGGGC 46

RESULT 8  
 AAA71100  
 ID AAA71100 standard; DNA; 46 BP.  
 XX  
 AC AAA71100;  
 XX  
 DT 27-APR-2001 (first entry)  
 XX  
 DE Molecular interaction site DNA #123.  
 XX  
 KW Modulator; identification; molecular interaction; virtual library; ss.

XX Unidentified.  
 OS  
 XX WO9958947-A2.  
 PN  
 XX 18-NOV-1999.  
 PD  
 XX 12-MAY-1999; 99WO-US010361.  
 PF  
 XX 12-MAY-1998; 98US-00076404.  
 PR  
 XX 12-MAY-1998; 98US-0085092P.  
 XX  
 PA (ISIS-) ISIS PHARM INC.  
 XX  
 XX Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;  
 PI Hofstadler S, Mcneil J;  
 XX  
 DR WPI; 2000-086439/07.  
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 PT used to provide compounds which can be used as pharmacological,  
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 XX Example 7; Fig 121; 405pp; English.

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 CC modulate the activity of a target biomolecule. The method uses 3-  
 CC dimensional representations of the biomolecule and a library of compounds  
 CC and comprises (a) identifying at least one molecular interaction site of  
 CC the target RNA; (b) generating in silico a virtual library of compounds  
 CC predicted or calculated to interact with the molecular interaction site;  
 CC and (c) comparing 3-dimensional (3-D) representations of the target RNA  
 CC with members of the virtual library of compounds to generate a hierarchy  
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 CC method also describes (1) RNA comprising a joined sequence of at least 24

CC nucleotides but not more than 70 nucleotides and having secondary  
 CC structure defined by: (a) 3 nucleotides forming a first side of a first  
 CC double stranded (ds) region; (b) 2 nucleotides forming a first side of an  
 CC internal loop region; (c) 4 nucleotides forming a first side of a second  
 CC ds region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4  
 CC nucleotides forming a second side of the second ds region; (f) 4  
 CC nucleotides forming a second side of the internal loop region; and (g) 3  
 CC nucleotides forming a second side of the first ds region; (2) a purified  
 CC and isolated RNA fragment comprising the human sequence  
 CC UUUACACAAUUAUCUUGUACAGAAAUUC (II). The methods and products can be  
 CC used for identifying agents which modulate the activity of biomolecules,  
 CC particularly RNA. Such agents can be used as pharmaceutical, agricultural  
 CC or industrial compounds  
 XX  
 SQ Sequence 46 BP; 11 A; 7 C; 9 G; 19 T; 0 U; 0 Other;

Query Match 96.6%; Score 28; DB 3; Length 46;  
 Best Local Similarity 60.7%; Pred. No. 0.0077;  
 Matches 17; Conservative 11; Mismatches 0; Indels 0; Gaps 0;

Qy 1 UAUGAUUCUUUUUGUAGCCUAGGGGC 28  
 :|||:||||:|||||:|||||  
 Db 19 TATGATCTTTTGTAGCCCTAGGGGC 46

RESULT 9  
 AAA71104  
 ID AAA71104 standard; RNA; 46 BP.  
 XX  
 AC AAA71104;  
 DT 27-APR-2001 (first entry)  
 XX  
 DE Molecular interaction site RNA #180.  
 XX  
 KW Modulator; identification; molecular interaction; virtual library; ss.  
 XX  
 OS Unidentified.  
 XX  
 PN WO9958947-A2.  
 XX  
 PD 18-NOV-1999.  
 XX  
 PF 12-MAY-1999; 99WO-US010361.  
 XX  
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 PR 12-MAY-1998; 98US-0085092P.  
 XX  
 PA (ISIS-) ISIS PHARM INC.  
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 PI Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;  
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 XX  
 DR WPI; 2000-086439/07.

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 PT used to provide compounds which can be used as pharmacological,  
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XX Example 7; Fig 122; 405pp; English.

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 CC modulate the activity of a target biomolecule. The method uses 3-  
 CC dimensional representations of the biomolecule and a library of compounds  
 CC and comprises (a) identifying at least one molecular interaction site of  
 CC the target RNA; (b) generating in silico a virtual library of compounds  
 CC predicted or calculated to interact with the molecular interaction site;  
 CC and (c) comparing 3-dimensional (3-D) representations of the target RNA  
 CC with members of the virtual library of compounds to generate a hierarchy  
 CC of the compounds ranked in accordance with their respective ability to  
 CC form physical interactions with the molecular interaction site. The  
 CC method also describes (1) RNA comprising a joined sequence of at least 24  
 CC nucleotides but not more than 70 nucleotides and having secondary

CC structure defined by: (a) 3 nucleotides forming a first side of a first  
 CC double stranded (ds) region; (b) 2 nucleotides forming a first side of an  
 CC internal loop region; (c) 4 nucleotides forming a first side of a second  
 CC ds region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4  
 CC nucleotides forming a second side of the second ds region; (f) 4  
 CC nucleotides forming a second side of the internal loop region; and (g) 3  
 CC nucleotides forming a second side of the first ds region; (2) a purified  
 CC and isolated RNA fragment comprising the human sequence  
 CC UUUACACAAUUAUCUUGUACAGAAAUUC (II). The methods and products can be  
 CC used for identifying agents which modulate the activity of biomolecules,  
 CC particularly RNA. Such agents can be used as pharmaceutical, agricultural  
 CC or industrial compounds  
 XX  
 SQ Sequence 46 BP; 11 A; 7 C; 9 G; 0 T; 19 U; 0 Other;

Query Match 96.6%; Score 28; DB 3; Length 46;  
 Best Local Similarity 100.0%; Pred. No. 0.0077;  
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 UAUGAUUCUUUUUGUAGCCUAGGGGC 28  
 :|||||:|||||:|||||:|||||  
 Db 19 UAUGAUUCUUUUUGUAGCCUAGGGGC 46

RESULT 10  
 AAA71113  
 ID AAA71113 standard; RNA; 42 BP.  
 XX  
 AC AAA71113;  
 DT 27-APR-2001 (first entry)  
 XX  
 DE Molecular interaction site RNA #189.  
 XX  
 KW Modulator; identification; molecular interaction; virtual library; ss.  
 XX  
 OS Unidentified.  
 XX  
 PN WO9958947-A2.  
 XX  
 PD 18-NOV-1999.  
 XX  
 PF 12-MAY-1999; 99WO-US010361.  
 XX  
 PR 12-MAY-1998; 98US-00076404.  
 PR 12-MAY-1998; 98US-0085092P.  
 XX  
 PA (ISIS-) ISIS PHARM INC.  
 XX  
 PI Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;  
 PI Hofstadler S, McNeil J;  
 XX  
 DR WPI; 2000-086439/07.

XX Identifying compounds which modulate activity of target biomolecules,  
 PT used to provide compounds which can be used as pharmacological,  
 PT agricultural and industrial compounds.

XX Example 7; Fig 122; 405pp; English.

XX This invention describes a novel method for identifying compounds which  
 CC modulate the activity of a target biomolecule. The method uses 3-  
 CC dimensional representations of the biomolecule and a library of compounds  
 CC and comprises (a) identifying at least one molecular interaction site of  
 CC the target RNA; (b) generating in silico a virtual library of compounds  
 CC predicted or calculated to interact with the molecular interaction site;  
 CC and (c) comparing 3-dimensional (3-D) representations of the target RNA  
 CC with members of the virtual library of compounds to generate a hierarchy  
 CC of the compounds ranked in accordance with their respective ability to  
 CC form physical interactions with the molecular interaction site. The  
 CC method also describes (1) RNA comprising a joined sequence of at least 24  
 CC nucleotides but not more than 70 nucleotides and having secondary  
 CC structure defined by: (a) 3 nucleotides forming a first side of a first



CC ds region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4  
 CC nucleotides forming a second side of the second ds region; (f) 4  
 CC nucleotides forming a second side of the internal loop region; and (g) 3  
 CC nucleotides forming a second side of the first ds region; (2) a purified  
 CC and isolated RNA fragment comprising the human sequence  
 CC UUUACACAAUAUCUAGUUUACAGAAAAC (II). The methods and products can be  
 CC used for identifying agents which modulate the activity of biomolecules,  
 CC particularly RNA. Such agents can be used as pharmaceutical, agricultural  
 CC or industrial compounds

XX  
 SQ Sequence 42 BP; 12 A; 7 C; 6 G; 0 T; 17 U; 0 Other;

Query Match 89.0%; Score 25.8; DB 3; Length 42;  
 Best Local Similarity 93.1%; Pred. No. 0.074; Mismatches 0; Gaps 0;  
 Matches 27; Conservative 0; Indels 2; Gaps 0;

QY 1 UAUAGUUUUUUUUAAGCCUAGGGGU 29  
 |||||  
 Db 4 UAUAGUUUUUUUUAAGCCUAGGGGU 32  
 |||||

## RESULT 13

AAA71085  
 ID AAA71085 standard; DNA; 46 BP.

AC AAA71085;

XX 27-APR-2001 (first entry)

XX Molecular interaction site DNA #108.

XX Modulator; identification; molecular interaction; virtual library; ss.

XX Unidentified.

XX WO9958947-A2.

XX 18-NOV-1999.

XX 12-MAY-1999; 99WO-US010361.

XX 12-MAY-1998; 98US-00076404.

XX 12-MAY-1998; 98US-0085092P.

XX (ISIS-) ISIS PHARM INC.

XX Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;

XX Hofstadler S, Mcneil J;

XX WPI; 2000-086439/07.

XX Identifying compounds which modulate activity of target biomolecules,  
 XX used to provide compounds which can be used as pharmaceutical,  
 XX agricultural and industrial compounds.

XX Example 7; Fig 121; 405pp; English.

XX This invention describes a novel method for identifying compounds which  
 XX modulate the activity of a target biomolecule. The method uses 3-  
 XX dimensional representations of the biomolecule and a library of compounds  
 XX and comprises (a) identifying at least one molecular interaction site of  
 XX the target RNA; (b) generating in silico a virtual library of compounds  
 XX predicted or calculated to interact with the molecular interaction site;  
 XX and (c) comparing 3-dimensional (3-D) representations of the target RNA  
 XX with members of the virtual library of compounds to generate a hierarchy  
 XX of the compounds ranked in accordance with their respective ability to  
 XX form physical interactions with the molecular interaction site. The  
 XX method also describes (1) RNA comprising a joined sequence of at least 24  
 XX nucleotides but not more than 70 nucleotides and having secondary  
 XX structure defined by: (a) 3 nucleotides forming a first side of a first  
 XX double stranded (ds) region; (b) 2 nucleotides forming a first side of an  
 XX internal loop region; (c) 4 nucleotides forming a first side of a second  
 XX ds region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4

CC nucleotides forming a second side of the second ds region; (f) 4  
 CC nucleotides forming a second side of the internal loop region; and (g) 3  
 CC nucleotides forming a second side of the first ds region; (2) a purified  
 CC and isolated RNA fragment comprising the human sequence  
 CC UUUACACAAUAUCUAGUUUACAGAAAAC (II). The methods and products can be  
 CC used for identifying agents which modulate the activity of biomolecules,  
 CC particularly RNA. Such agents can be used as pharmaceutical, agricultural  
 CC or industrial compounds

XX  
 SQ Sequence 46 BP; 12 A; 7 C; 9 G; 18 T; 0 U; 0 Other;

Query Match 85.5%; Score 24.8; DB 3; Length 46;

Best Local Similarity 57.1%; Pred. No. 0.21;

Matches 16; Conservative 10; Mismatches 2; Indels 0; Gaps 0;

QY 1 UAUAGUUUUUUUUAAGCCUAGGGGC 28  
 :|||:|||||:|||||:|||||

Db 19 TAAAGATCTTTTGTAGCCCTACGGGC 46

## RESULT 14

AAA71103

ID AAA71103 standard; RNA; 46 BP.

AC AAA71103;

XX 27-APR-2001 (first entry)

XX Molecular interaction site RNA #179.

XX Modulator; identification; molecular interaction; virtual library; ss.

XX Unidentified.

XX WO9958947-A2.

XX 18-NOV-1999.

XX 12-MAY-1999; 99WO-US010361.

XX 12-MAY-1998; 98US-00076404.

XX 12-MAY-1998; 98US-0085092P.

XX (ISIS-) ISIS PHARM INC.

XX Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;

XX Hofstadler S, Mcneil J;

XX WPI; 2000-086439/07.

XX Identifying compounds which modulate activity of target biomolecules,  
 XX used to provide compounds which can be used as pharmaceutical,  
 XX agricultural and industrial compounds.

XX Example 7; Fig 122; 405pp; English.

XX This invention describes a novel method for identifying compounds which  
 XX modulate the activity of a target biomolecule. The method uses 3-  
 XX dimensional representations of the biomolecule and a library of compounds  
 XX and comprises (a) identifying at least one molecular interaction site of  
 XX the target RNA; (b) generating in silico a virtual library of compounds  
 XX predicted or calculated to interact with the molecular interaction site;  
 XX and (c) comparing 3-dimensional (3-D) representations of the target RNA  
 XX with members of the virtual library of compounds to generate a hierarchy  
 XX of the compounds ranked in accordance with their respective ability to  
 XX form physical interactions with the molecular interaction site. The  
 XX method also describes (1) RNA comprising a joined sequence of at least 24  
 XX nucleotides but not more than 70 nucleotides and having secondary  
 XX structure defined by: (a) 3 nucleotides forming a first side of a first  
 XX double stranded (ds) region; (b) 2 nucleotides forming a first side of an  
 XX internal loop region; (c) 4 nucleotides forming a first side of a second  
 XX ds region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4  
 XX nucleotides forming a second side of the second ds region; (f) 4

CC nucleotides forming a second side of the internal loop region; and (g) 3  
CC nucleotides forming a second side of the first ds region; (2) a purified  
CC and isolated RNA fragment comprising the human sequence  
CC UUUACAACAUUAUAGUUUACAGAAAUC (II). The methods and products can be  
CC used for identifying agents which modulate the activity of biomolecules,  
CC particularly RNA. Such agents can be used as pharmaceutical, agricultural  
CC or industrial compounds

XX Sequence 46 BP; 12 A; 7 C; 9 G; 0 T; 18 U; 0 Other;  
SQ

Query Match 85.5%; Score 24.8; DB 3; Length 46;  
Best Local Similarity 92.9%; Pred. No. 0.21;  
Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 UAUGAUCUUCUUUGUAAGCCUAGGGC 28  
DB 19 UAAGAUCUUCUUUGUAAGCCUAGGGC 46

## RESULT 15

AAA71114  
ID AAA71114 standard; RNA; 42 BP.

XX  
AC AAA71114;

DT 27-APR-2001 (first entry)

DE Molecular interaction site RNA #190.

XX Modulator; identification; molecular interaction; virtual library; ss.

XX Unidentified.

XX WO958947-A2.

XX 18-NOV-1999.

XX 12-MAY-1999; 99WO-US010361.

XX 12-MAY-1998; 98US-00076404.

XX 12-MAY-1998; 98US-0085092P.

XX (ISIS-) ISIS PHARM INC.

XX Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;  
PI Hofstadler S, Mcneil J;

XX WPI; 2000-086439/07.

XX Identifying compounds which modulate activity of target biomolecules,  
PT used to provide compounds which can be used as pharmacological,  
PT agricultural and industrial compounds.

XX Example 7; Fig 122; 405pp; English.

XX This invention describes a novel method for identifying compounds which  
CC modulate the activity of a target biomolecule. The method uses 3-  
CC dimensional representations of the biomolecule and a library of compounds  
CC and comprises (a) identifying at least one molecular interaction site of  
CC the target RNA; (b) generating in silico a virtual library of compounds  
CC predicted or calculated to interact with the molecular interaction site;  
CC and (c) comparing 3-dimensional (3-D) representations of the target RNA  
CC with members of the virtual library of compounds to generate a hierarchy  
CC of the compounds ranked in accordance with their respective ability to  
CC form physical interactions with the molecular interaction site. The  
CC method also describes (1) RNA comprising a joined sequence of at least 24  
CC nucleotides but not more than 70 nucleotides and having secondary  
CC structure defined by: (a) 3 nucleotides forming a first side of a first  
CC double stranded (ds) region; (b) 2 nucleotides forming a first side of an  
CC internal loop region; (c) 4 nucleotides forming a first side of a second  
CC ds region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4  
CC nucleotides forming a second side of the second ds region; (f) 4  
CC nucleotides forming a second side of the internal loop region; and (g) 3  
CC nucleotides forming a second side of the first ds region; (2) a purified

CC nucleotides forming a second side of the first ds region; (2) a purified  
CC and isolated RNA fragment comprising the human sequence  
CC UUUACAACAUUAUAGUUUACAGAAAUC (II). The methods and products can be  
CC used for identifying agents which modulate the activity of biomolecules,  
CC particularly RNA. Such agents can be used as pharmaceutical, agricultural  
CC or industrial compounds

XX Sequence 42 BP; 11 A; 8 C; 7 G; 0 T; 16 U; 0 Other;  
SQ

Query Match 82.1%; Score 23.8; DB 3; Length 42;  
Best Local Similarity 92.6%; Pred. No. 0.58;  
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 UAUGAUCUUCUUUGUAAGCCUAGGGC 27  
DB 4 UAAGAUCUUCUUUGUAAGCCUAGGGC 30

## RESULT 16

AAA71119

ID AAA71119 standard; DNA; 42 BP.

XX  
AC AAA71119;

DT 27-APR-2001 (first entry)

DE Molecular interaction site DNA #125.

XX Modulator; identification; molecular interaction; virtual library; ss.

XX Unidentified.

XX WO958947-A2.

XX 18-NOV-1999.

XX 12-MAY-1999; 99WO-US010361.

XX 12-MAY-1998; 98US-00076404.

XX 12-MAY-1998; 98US-0085092P.

XX (ISIS-) ISIS PHARM INC.

XX Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;  
PI Hofstadler S, Mcneil J;

XX WPI; 2000-086439/07.

XX Identifying compounds which modulate activity of target biomolecules,  
PT used to provide compounds which can be used as pharmacological,  
PT agricultural and industrial compounds.

XX Example 7; Fig 125; 405pp; English.

XX This invention describes a novel method for identifying compounds which  
CC modulate the activity of a target biomolecule. The method uses 3-  
CC dimensional representations of the biomolecule and a library of compounds  
CC and comprises (a) identifying at least one molecular interaction site of  
CC the target RNA; (b) generating in silico a virtual library of compounds  
CC predicted or calculated to interact with the molecular interaction site;  
CC and (c) comparing 3-dimensional (3-D) representations of the target RNA  
CC with members of the virtual library of compounds to generate a hierarchy  
CC of the compounds ranked in accordance with their respective ability to  
CC form physical interactions with the molecular interaction site. The  
CC method also describes (1) RNA comprising a joined sequence of at least 24  
CC nucleotides but not more than 70 nucleotides and having secondary  
CC structure defined by: (a) 3 nucleotides forming a first side of a first  
CC double stranded (ds) region; (b) 2 nucleotides forming a first side of an  
CC internal loop region; (c) 4 nucleotides forming a first side of a second  
CC ds region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4  
CC nucleotides forming a second side of the second ds region; (f) 4  
CC nucleotides forming a second side of the internal loop region; and (g) 3  
CC nucleotides forming a second side of the first ds region; (2) a purified

CC and isolated RNA fragment comprising the human sequence  
CC UUACACAAUAUCUAGUUUACAGAAAAUC (II). The methods and products can be  
CC used for identifying agents which modulate the activity of biomolecules,  
CC particularly RNA. Such agents can be used as pharmaceutical, agricultural  
CC or industrial compounds

XX  
SQ Sequence 42 BP; 11 A; 8 C; 7 G; 16 T; 0 U; 0 Other;  
Query Match 82.1%; Score 23.8; DB 3; Length 42;  
Best Local Similarity 55.6%; Pred. No. 0.58;  
Matches 15; Conservative 10; Mismatches 2; Indels 0; Gaps 0;

QY 1 UAUAUUCUUUUUGUAGCCCUAGGGG 27  
: |||||:|||||:|||||:|||||:  
Db 4 TAGATTCTTTTGTAAAGCCCTAGGCG 30

RESULT 17  
AAA71127  
ID AAA71127 standard; RNA; 42 BP.  
XX  
AC AAA71127;  
XX  
DT 27-APR-2001 (first entry)  
XX  
DE Molecular interaction site RNA #196.  
XX  
KW Modulator; identification; molecular interaction; virtual library; ss.  
XX  
OS Unidentified.  
XX  
PN WO9958947-A2.  
XX  
PD 18-NOV-1999.  
XX  
PF 12-MAY-1999; 99WO-US010361.  
XX  
PR 12-MAY-1998; 98US-00076404.  
XX  
PR 12-MAY-1998; 98US-0085092P.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;  
PI Hofstadler S, McNeil J;  
XX  
DR WPI; 2000-086439/07.  
XX  
PT Identifying compounds which modulate activity of target biomolecules,  
PT used to provide compounds which can be used as pharmacological,  
PT agricultural and industrial compounds.  
XX  
PS Example 7; Fig 126; 405pp; English.

XX This invention describes a novel method for identifying compounds which  
CC modulate the activity of a target biomolecule. The method uses 3-  
CC dimensional representations of the biomolecule and a library of compounds  
CC and comprises (a) identifying at least one molecular interaction site of  
CC the target RNA; (b) generating in silico a virtual library of compounds  
CC predicted or calculated to interact with the molecular interaction site;  
CC and (c) comparing 3-dimensional (3-D) representations of the target RNA  
CC with members of the virtual library of compounds to generate a hierarchy  
CC of the compounds ranked in accordance with their respective ability to  
CC form physical interactions with the molecular interaction site. The  
CC method also describes (1) RNA comprising a joined sequence of at least 24  
CC nucleotides but not more than 70 nucleotides and having secondary  
CC structure defined by: (a) 3 nucleotides forming a first side of a first  
CC double stranded (ds) region; (b) 2 nucleotides forming a first side of an  
CC internal loop region; (c) 4 nucleotides forming a first side of a second  
CC ds region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4  
CC nucleotides forming a second side of the second ds region; (f) 4  
CC nucleotides forming a second side of the internal loop region; and (g) 3  
CC nucleotides forming a second side of the first ds region; (2) a purified  
CC and isolated RNA fragment comprising the human sequence

CC UUACACAAUAUCUAGUUUACAGAAAAUC (II). The methods and products can be  
CC used for identifying agents which modulate the activity of biomolecules,  
CC particularly RNA. Such agents can be used as pharmaceutical, agricultural  
CC or industrial compounds

XX  
SQ Sequence 42 BP; 11 A; 8 C; 7 G; 0 T; 16 U; 0 Other;  
Query Match 82.1%; Score 23.8; DB 3; Length 42;  
Best Local Similarity 92.6%; Pred. No. 0.58;  
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 UAUAUUCUUUUUGUAGCCCUAGGGG 27  
: |||||:|||||:|||||:|||||:  
Db 4 UAUAUUCUUUUUGUAGCCCUAGGGG 30

RESULT 18  
AAA71094  
ID AAA71094 standard; DNA; 46 BP.  
XX  
AC AAA71094;  
XX  
DT 27-APR-2001 (first entry)  
XX  
DE Molecular interaction site DNA #117.  
XX  
KW Modulator; identification; molecular interaction; virtual library; ss.  
XX  
OS Unidentified.  
XX  
PN WO9958947-A2.  
XX  
PD 18-NOV-1999.  
XX  
PF 12-MAY-1999; 99WO-US010361.  
XX  
PR 12-MAY-1998; 98US-00076404.  
XX  
PR 12-MAY-1998; 98US-0085092P.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;  
PI Hofstadler S, McNeil J;  
XX  
DR WPI; 2000-086439/07.  
XX  
PT Identifying compounds which modulate activity of target biomolecules,  
PT used to provide compounds which can be used as pharmacological,  
PT agricultural and industrial compounds.  
XX  
PS Example 7; Fig 121; 405pp; English.

XX This invention describes a novel method for identifying compounds which  
CC modulate the activity of a target biomolecule. The method uses 3-  
CC dimensional representations of the biomolecule and a library of compounds  
CC and comprises (a) identifying at least one molecular interaction site of  
CC the target RNA; (b) generating in silico a virtual library of compounds  
CC predicted or calculated to interact with the molecular interaction site;  
CC and (c) comparing 3-dimensional (3-D) representations of the target RNA  
CC with members of the virtual library of compounds to generate a hierarchy  
CC of the compounds ranked in accordance with their respective ability to  
CC form physical interactions with the molecular interaction site. The  
CC method also describes (1) RNA comprising a joined sequence of at least 24  
CC nucleotides but not more than 70 nucleotides and having secondary  
CC structure defined by: (a) 3 nucleotides forming a first side of a first  
CC double stranded (ds) region; (b) 2 nucleotides forming a first side of an  
CC internal loop region; (c) 4 nucleotides forming a first side of a second  
CC ds region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4  
CC nucleotides forming a second side of the second ds region; (f) 4  
CC nucleotides forming a second side of the internal loop region; and (g) 3  
CC nucleotides forming a second side of the first ds region; (2) a purified  
CC and isolated RNA fragment comprising the human sequence

UUACACAAUAUCUAGUUUACAGAAAAUC (II). The methods and products can be





```
CC or industrial compounds
XX SQ Sequence 29 BP; 8 A; 6 C; 6 G; 0 T; 9 U; 0 Other;
Query Match 80.0%; Score 23.2; DB 3; Length 29;
Best Local Similarity 89.3%; Pred. No. 1;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 AUGAUCUUUUUGAAGCCCGGCGCU 29
Db 2 AAGAUCUUUUUGAAGCCCGGCGCU 29

RESULT 21
AA70830
ID AAA70830 standard; RNA; 29 BP.
XX AC AAA70830;
XX DT 27-APR-2001 (first entry)
XX DE Molecular interaction site RNA #30.
XX KW Modulator; identification; molecular interaction; virtual library; ss.
XX OS Rattus sp.
XX PN WO958947-A2.
XX PD 18-NOV-1999.
XX PF 12-MAY-1999; 99WO-US010361.
XX PR 12-MAY-1998; 98US-00076404.
XX PR 12-MAY-1998; 98US-0085092P.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;
PI Hofstadler S, Mcneil J;
XX WPI; 2000-086439/07.
XX PT Identifying compounds which modulate activity of target biomolecules,
XX PT used to provide compounds which can be used as pharmacological,
XX PT agricultural and industrial compounds.
XX PS Claim 235; Page 235; 405pp; English.
XX CC This invention describes a novel method for identifying compounds which
XX CC modulate the activity of a target biomolecule. The method uses 3-
XX CC dimensional representations of the biomolecule and a library of compounds
XX CC and comprises (a) identifying at least one molecular interaction site of
XX CC the target RNA; (b) generating in silico a virtual library of compounds
XX CC predicted or calculated to interact with the molecular interaction site;
XX CC and (c) comparing 3-dimensional (3-D) representations of the target RNA
XX CC with members of the virtual library of compounds to generate a hierarchy
XX CC of the compounds ranked in accordance with their respective ability to
XX CC form physical interactions with the molecular interaction site. The
XX CC method also describes (1) RNA comprising a joined sequence of at least 24
XX CC nucleotides but not more than 70 nucleotides and having secondary
XX CC structure defined by: (a) 3 nucleotides forming a first side of a first
XX CC double stranded (ds) region; (b) 2 nucleotides forming a first side of an
XX CC internal loop region; (c) 4 nucleotides forming a first side of a second
XX CC ds region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4
XX CC nucleotides forming a second side of the second ds region; (f) 4
XX CC nucleotides forming a second side of the internal loop region; and (g) 3
XX CC nucleotides forming a second side of the first ds region; (2) a purified
XX CC and isolated RNA fragment comprising the human sequence
XX CC UUUACACAAUACUUGUACAGAAAUC (II). The methods and products can be
XX CC used for identifying agents which modulate the activity of biomolecules,
XX CC particularly RNA. Such agents can be used as pharmaceutical, agricultural
XX CC or industrial compounds
```

```
XX SQ Sequence 29 BP; 8 A; 6 C; 6 G; 0 T; 9 U; 0 Other;
Query Match 80.0%; Score 23.2; DB 3; Length 29;
Best Local Similarity 89.3%; Pred. No. 1;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 AUGAUCUUUUUGAAGCCCGGCGCU 29
Db 2 AAGAUCUUUUUGAAGCCCGGCGCU 29

RESULT 22
AAA71121
ID AAA71121 standard; DNA; 42 BP.
XX AC AAA71121;
XX DT 27-APR-2001 (first entry)
XX DE Molecular interaction site DNA #127.
XX KW Modulator; identification; molecular interaction; virtual library; ss.
XX OS Unidentified.
XX PN WO958947-A2.
XX PD 18-NOV-1999.
XX PF 12-MAY-1999; 99WO-US010361.
XX PR 12-MAY-1998; 98US-00076404.
XX PR 12-MAY-1998; 98US-0085092P.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;
PI Hofstadler S, Mcneil J;
XX WPI; 2000-086439/07.
XX PT Identifying compounds which modulate activity of target biomolecules,
XX PT used to provide compounds which can be used as pharmacological,
XX PT agricultural and industrial compounds.
XX PS Example 7; Fig 125; 405pp; English.
XX CC This invention describes a novel method for identifying compounds which
XX CC modulate the activity of a target biomolecule. The method uses 3-
XX CC dimensional representations of the biomolecule and a library of compounds
XX CC and comprises (a) identifying at least one molecular interaction site of
XX CC the target RNA; (b) generating in silico a virtual library of compounds
XX CC predicted or calculated to interact with the molecular interaction site;
XX CC and (c) comparing 3-dimensional (3-D) representations of the target RNA
XX CC with members of the virtual library of compounds to generate a hierarchy
XX CC of the compounds ranked in accordance with their respective ability to
XX CC form physical interactions with the molecular interaction site. The
XX CC method also describes (1) RNA comprising a joined sequence of at least 24
XX CC nucleotides but not more than 70 nucleotides and having secondary
XX CC structure defined by: (a) 3 nucleotides forming a first side of a first
XX CC double stranded (ds) region; (b) 2 nucleotides forming a first side of an
XX CC internal loop region; (c) 4 nucleotides forming a first side of a second
XX CC ds region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4
XX CC nucleotides forming a second side of the second ds region; (f) 4
XX CC nucleotides forming a second side of the internal loop region; and (g) 3
XX CC nucleotides forming a second side of the first ds region; (2) a purified
XX CC and isolated RNA fragment comprising the human sequence
XX CC UUUACACAAUACUUGUACAGAAAUC (II). The methods and products can be
XX CC used for identifying agents which modulate the activity of biomolecules,
XX CC particularly RNA. Such agents can be used as pharmaceutical, agricultural
XX CC or industrial compounds
```



```

Best Local Similarity 89.3%; Pred. No. 1.1;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AUGAUCUUUUUGUAAGCCCUAGGGGCU 29
      |||||
Db 5 AAGAUCUUUUUGUAAGCCCAAGGGCU 32
      |||||

```

RESULT 26  
AAA71115  
ID AAA71115 standard; RNA; 42 BP.  
XX XX  
AC AAA71115;                     
XX XX  
DT 27-APR-2001 (first entry)     
XX XX  
DE Molecular interaction site RNA #191.  
XX XX  
KW Modulator; identification; molecular interaction; virtual library; ss.  
XX XX  
OS Unidentified.

|    |   |                |
|----|---|----------------|
| PD | 18-NOV-1999.  |                |
| XX |   |                |
| XX | 12-MAY-1999;  | 99WC-US010361. |
| PF |   |                |
| XX |   |                |
| XX | 12-MAY-1998;  | 98US-00076404. |
| PR |   |                |
| XX | 12-MAY-1998;  | 98US-0085092P. |
| PR |   |                |
| XX | (ISIS-) ISIS PHARM INC.   |                |
| XX |   |                |
| FA |   |                |
| XX | Ecker DJ, Griffey R, Croke ST, Sampath R, Swayze E, Mohan V;          |                |
| XX | Hofstadler S, Mcneil J;   |                |
| PI |   |                |
| PI | WPI; 2000-086439/07.  |                |
| XX |   |                |
| XX |   |                |
| DR |   |                |
| XX |   |                |
| XX | Identifying compounds which modulate activity of target biomolecules, |                |
| PT | used to provide compounds which can be used as pharmacological,       |                |
| PT | agricultural and industrial compounds.                                |                |
| PT |   |                |
| XX |   |                |
| XX | Example 7; Fig 122; 405pp; English.                                   |                |
| PS |   |                |

This invention describes a novel method for identifying compounds which modulate the activity of a target biomolecule. The method uses 3-dimensional representations of the biomolecule and a library of compounds and comprises (a) identifying at least one molecular interaction site of the target RNA; (b) generating *in silico* a virtual library of compounds predicted or calculated to interact with the molecular interaction site; and (c) comparing 3-dimensional (3-D) representations of the target RNA with members of the virtual library of compounds to generate a hierarchy of the compounds ranked in accordance with their respective ability to form physical interactions with the molecular interaction site. The method also describes (1) RNA comprising a joined sequence of at least 24 nucleotides but not more than 70 nucleotides and having secondary structure defined by: (a) 3 nucleotides forming a first side of a first internal loop region; (c) 4 nucleotides forming a first side of a second internal loop region; (c) 4 nucleotides forming an end loop region; (e) 4 nucleotides forming a second side of the second ds region; (f) 4 nucleotides forming a second side of the internal loop region; and (g) 3 nucleotides forming a second side of the first ds region; (2) a purified and isolated RNA fragment comprising the human sequence UUUACAAUACUAGUUUACAGAAAUC (iii). The methods and products can be used for identifying agents which modulate the activity of biomolecules, particularly RNA. Such agents can be used as pharmaceutical, agricultural or industrial compounds.

AA Sequence 42 BP; 13 A; 7 C; 7 G; 0 T; 15 U; 0 Other;  
SQ Query Match 80.0%; Score 23.2; DB 3; Length 42;  
Best Local Similarity 89.3%; Pred. No. 1.1;  
Pred. No. 1.1;

Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AUGAUCUUUUUGUAGCCCUAGGGCU 29  
| | | | | | | | | | | | | | | | | | | | |  
Db 5 AAGAUCUUUUUGUAGCCCUAGGGCU 32

## RESULT 27

AAA71129  
ID AAA71129 standard; RNA; 42 BP.

XX  
AC AAA71129;  
XX

DT 27-APR-2001 (first entry)

DE Molecular interaction site RNA #198.

XX Modulator; identification; molecular interaction; virtual library; ss.

OS Unidentified.

XX  
PN WO9958947-A2.

XX  
PD 18-NOV-1999.

XX  
PF 12-MAY-1999; 99WO-US010361.

XX  
PR 12-MAY-1998; 98US-00076404.

XX  
PR 12-MAY-1998; 98US-0085092P.

XX (ISIS-) ISIS PHARM INC.

XX Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;

PI Hofstadler S, Mcneil J;

XX  
DR WPI; 2000-086439/07.

XX Identifying compounds which modulate activity of target biomolecules,  
PT used to provide compounds which can be used as pharmacological,  
PT agricultural and industrial compounds.

XX Example 7; Fig 126; 405pp; English.

XX This invention describes a novel method for identifying compounds which  
modulate the activity of a target biomolecule. The method uses 3-  
dimensional representations of the biomolecule and a library of compounds  
and comprises (a) identifying at least one molecular interaction site of  
the target RNA; (b) generating in silico a virtual library of compounds  
predicted or calculated to interact with the molecular interaction site;  
and (c) comparing 3-dimensional (3-D) representations of the target RNA  
with members of the virtual library of compounds to generate a hierarchy  
of the compounds ranked in accordance with their respective ability to  
form physical interactions with the molecular interaction site. The  
method also describes (1) RNA comprising a joined sequence of at least 24  
nucleotides but not more than 70 nucleotides and having secondary  
structure defined by: (a) 3 nucleotides forming a first side of a first  
double stranded (ds) region; (b) 2 nucleotides forming a first side of an  
internal loop region; (c) 4 nucleotides forming a first side of a second  
ds region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4  
nucleotides forming a second side of the second ds region; (f) 4  
nucleotides forming a second side of the internal loop region; and (g) 3  
nucleotides forming a second side of the first ds region; (2) a purified  
and isolated RNA fragment comprising the human sequence  
UUUACACAUUAUCUUAUACAGAAAUC (II). The methods and products can be  
used for identifying agents which modulate the activity of biomolecules,  
particularly RNA. Such agents can be used as pharmaceutical, agricultural  
or industrial compounds

XX Sequence 42 BP; 13 A; 7 C; 7 G; 0 T; 15 U; 0 Other;

Query Match 80.0%; Score 23.2; DB 3; Length 42;  
Best Local Similarity 89.3%; Pred. No. 1.1;  
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AUGAUCUUUUUGUAGCCCUAGGGCU 29  
| | | | | | | | | | | | | | | | | | | | |  
Db 5 AAGAUCUUUUUGUAGCCCUAGGGCU 32

## RESULT 28

AAA71124  
ID AAA71124 standard; DNA; 42 BP.

XX  
AC AAA71124;

DT 27-APR-2001 (first entry)

DE Molecular interaction site DNA #130.

XX Modulator; identification; molecular interaction; virtual library; ss.

OS Unidentified.

XX  
PN WO9958947-A2.

XX  
PD 18-NOV-1999.

XX  
PF 12-MAY-1999; 99WO-US010361.

XX  
PR 12-MAY-1998; 98US-00076404.

XX  
PR 12-MAY-1998; 98US-0085092P.

XX (ISIS-) ISIS PHARM INC.

XX Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;

PI Hofstadler S, Mcneil J;

XX  
DR WPI; 2000-086439/07.

XX Identifying compounds which modulate activity of target biomolecules,  
PT used to provide compounds which can be used as pharmacological,  
PT agricultural and industrial compounds.

XX Example 7; Fig 125; 405pp; English.

XX This invention describes a novel method for identifying compounds which  
modulate the activity of a target biomolecule. The method uses 3-  
dimensional representations of the biomolecule and a library of compounds  
and comprises (a) identifying at least one molecular interaction site of  
the target RNA; (b) generating in silico a virtual library of compounds  
predicted or calculated to interact with the molecular interaction site;  
and (c) comparing 3-dimensional (3-D) representations of the target RNA  
with members of the virtual library of compounds to generate a hierarchy  
of the compounds ranked in accordance with their respective ability to  
form physical interactions with the molecular interaction site. The  
method also describes (1) RNA comprising a joined sequence of at least 24  
nucleotides but not more than 70 nucleotides and having secondary  
structure defined by: (a) 3 nucleotides forming a first side of a first  
double stranded (ds) region; (b) 2 nucleotides forming a first side of an  
internal loop region; (c) 4 nucleotides forming a first side of a second  
ds region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4  
nucleotides forming a second side of the second ds region; (f) 4  
nucleotides forming a second side of the internal loop region; and (g) 3  
nucleotides forming a second side of the first ds region; (2) a purified  
and isolated RNA fragment comprising the human sequence  
UUUACACAUUAUCUUAUACAGAAAUC (II). The methods and products can be  
used for identifying agents which modulate the activity of biomolecules,  
particularly RNA. Such agents can be used as pharmaceutical, agricultural  
or industrial compounds

XX Sequence 42 BP; 11 A; 10 C; 7 G; 14 T; 0 U; 0 Other;

Query Match 77.9%; Score 22.6; DB 3; Length 42;  
Best Local Similarity 51.7%; Pred. No. 2;  
Matches 15; Conservative 10; Mismatches 4; Indels 0; Gaps 0;



Db 19 AAGAUCUUUUGUAAGCCCCAAGGC 45

20 A G A T T C T T T T T G T A G C C C C A A G G C C 46

RESULT 33  
AAA71106  
ID AAA71106 standard; RNA; 46 BP.  
XX AC  
XX AAA71106;  
DT 27-APR-2001 (first entry)  
XX DE  
XX Molecular interaction site RNA #182.  
XX KW  
XX Modulator; identification; molecular interaction; virtual library; ss.  
XX OS  
XX Unidentified.  
XX PN  
XX WO9958947-A2.  
XX PD  
XX 18-NOV-1999.  
XX PF  
XX 12-MAY-1999; 99WO-US010361.  
XX PR  
XX 12-MAY-1998; 98US-00076404.  
XX PR  
XX 12-MAY-1998; 98US-0085092P.  
XX XX  
XX (ISIS-) ISIS PHARM INC.  
XX PA  
XX Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;  
XX PI  
XX Hofstadler S, Mcneil J;  
XX PI  
XX WPI; 2000-086439/07.  
XX DR  
XX  
XX Identifying compounds which modulate activity of target biomolecules,  
XX PT  
XX used to provide compounds which can be used as pharmacological,  
XX PT  
XX agricultural and industrial compounds.  
XX XX  
XX Example 7; Fig 122; 405pp; English.  
XX XX  
XX This invention describes a novel method for identifying compounds which  
XX CC  
XX modulate the activity of a target biomolecule. The method uses 3-  
XX CC  
XX dimensional representations of the biomolecule and a library of compounds  
XX CC  
XX and comprises (a) identifying at least one molecular interaction site of  
XX CC  
XX the target RNA; (b) generating in silico a virtual library of compounds  
XX CC  
XX predicted or calculated to interact with the molecular interaction site;  
XX CC  
XX and (c) comparing 3-dimensional (3-D) representations of the target RNA  
XX CC  
XX with members of the virtual library of compounds to generate a hierarchy  
XX CC  
XX of the compounds ranked in accordance with their respective ability to  
XX CC  
XX form physical interactions with the molecular interaction site. The  
XX CC  
XX method also describes (1) RNA comprising a joined sequence of at least 24  
XX CC  
XX nucleotides but not more than 70 nucleotides and having secondary  
XX CC  
XX structure defined by: (a) 3 nucleotides forming a first side of a first  
XX CC  
XX double stranded (ds) region; (b) 2 nucleotides forming a first side of an  
XX CC  
XX internal loop region; (c) 4 nucleotides forming a first side of a second  
XX CC  
XX ds region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4  
XX CC  
XX nucleotides forming a second side of the second ds region; (f) 4  
XX CC  
XX nucleotides forming a second side of the internal loop region; and (g) 3  
XX CC  
XX nucleotides forming a second side of the first ds region; (2) a purified  
XX CC  
XX and isolated RNA fragment comprising the human sequence  
XX CC  
XX UUUACACAAUUAUUAUUAAGCCUAGGGGC (II). The methods and products can be  
XX CC  
XX used for identifying agents which modulate the activity of biomolecules,  
XX CC  
XX particularly RNA. Such agents can be used as pharmaceutical, agricultural  
XX CC  
XX or industrial compounds  
XX SQ  
XX Sequence 46 BP; 14 A; 7 C; 9 G; 0 T; 16 U; 0 Other;

Query Match 76.6%; Score 22.2; DB 3; Length 46;  
Best Local Similarity 88.9%; Pred. No. 3.1;  
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2 AUGAUUCUUUUUUAAGCCUAGGGGC 28  
DB 20 AAGAUCUUUUUUAAGCCUAGGGGC 46

RESULT 35

RESULT 34  
AAA71107  
ID AAA71107 standard; RNA; 46 BP.  
XX AC  
XX AAA71107;  
DT 27-APR-2001 (first entry)  
XX DE  
XX Molecular interaction site RNA #183.  
XX KW  
XX Modulator; identification; molecular interaction; virtual library; ss.  
XX OS  
XX Unidentified.  
XX PN  
XX WO9958947-A2.  
XX PD  
XX 18-NOV-1999.  
XX PF  
XX 12-MAY-1999; 99WO-US010361.  
XX PR  
XX 12-MAY-1998; 98US-00076404.  
XX PR  
XX 12-MAY-1998; 98US-0085092P.  
XX XX  
XX (ISIS-) ISIS PHARM INC.  
XX PA  
XX Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;  
XX PI  
XX Hofstadler S, Mcneil J;  
XX PI  
XX WPI; 2000-086439/07.  
XX DR  
XX  
XX Identifying compounds which modulate activity of target biomolecules,  
XX PT  
XX used to provide compounds which can be used as pharmacological,  
XX PT  
XX agricultural and industrial compounds.  
XX XX  
XX Example 7; Fig 122; 405pp; English.

This invention describes a novel method for identifying compounds which  
XX CC  
XX modulate the activity of a target biomolecule. The method uses 3-  
XX CC  
XX dimensional representations of the biomolecule and a library of compounds  
XX CC  
XX and comprises (a) identifying at least one molecular interaction site of  
XX CC  
XX the target RNA; (b) generating in silico a virtual library of compounds  
XX CC  
XX predicted or calculated to interact with the molecular interaction site;  
XX CC  
XX and (c) comparing 3-dimensional (3-D) representations of the target RNA  
XX CC  
XX with members of the virtual library of compounds to generate a hierarchy  
XX CC  
XX of the compounds ranked in accordance with their respective ability to  
XX CC  
XX form physical interactions with the molecular interaction site. The  
XX CC  
XX method also describes (1) RNA comprising a joined sequence of at least 24  
XX CC  
XX nucleotides but not more than 70 nucleotides and having secondary  
XX CC  
XX structure defined by: (a) 3 nucleotides forming a first side of a first  
XX CC  
XX double stranded (ds) region; (b) 2 nucleotides forming a first side of an  
XX CC  
XX internal loop region; (c) 4 nucleotides forming a first side of a second  
XX CC  
XX ds region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4  
XX CC  
XX nucleotides forming a second side of the second ds region; (f) 4  
XX CC  
XX nucleotides forming a second side of the internal loop region; and (g) 3  
XX CC  
XX nucleotides forming a second side of the first ds region; (2) a purified  
XX CC  
XX and isolated RNA fragment comprising the human sequence  
XX CC  
XX UUUACACAAUUAUUAUUAAGCCUAGGGGC (II). The methods and products can be  
XX CC  
XX used for identifying agents which modulate the activity of biomolecules,  
XX CC  
XX particularly RNA. Such agents can be used as pharmaceutical, agricultural  
XX CC  
XX or industrial compounds  
XX SQ  
XX Sequence 46 BP; 14 A; 7 C; 9 G; 0 T; 16 U; 0 Other;

Query Match 76.6%; Score 22.2; DB 3; Length 46;  
Best Local Similarity 88.9%; Pred. No. 3.1;  
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2 AUGAUUCUUUUUUAAGCCUAGGGGC 28  
DB 20 AAGAUCUUUUUUAAGCCUAGGGGC 46



```
AAA71088
ID AAA71088 standard; DNA; 46 BP.
XX
AC
XX AAA71088;
XX
DT 27-APR-2001 (first entry)
XX
DE Molecular interaction site DNA #11.
XX
KW Modulator; identification; molecular interaction; virtual library; ss.
XX
OS Unidentified.
XX
FN WO9958947-A2.
XX
PD 18-NOV-1999.
XX
PF 12-MAY-1999; 99WO-US010361.
XX
PR 12-MAY-1998; 98US-00076404.
XX
PR 12-MAY-1998; 98US-0085092P.
XX
PA (ISIS-) ISIS PHARM INC.
XX
XX Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;
PI Hofstadler S, Mcneil J;
XX
XX WPI; 2000-086439/07.
XX
XX Identifying compounds which modulate activity of target biomolecules,
PT used to provide compounds which can be used as pharmacological,
PT agricultural and industrial compounds.
XX
XX Example 7; Fig 121; 405pp; English.
XX
XX This invention describes a novel method for identifying compounds which
CC modulate the activity of a target biomolecule. The method uses 3-
CC dimensional representations of the biomolecule and a library of compounds
CC and comprises (a) identifying at least one molecular interaction site of
CC the target RNA; (b) generating in silico a virtual library of compounds
CC predicted or calculated to interact with the molecular interaction site;
CC and (c) comparing 3-dimensional (3-D) representations of the target RNA
CC with members of the virtual library of compounds to generate a hierarchy
CC of the compounds ranked in accordance with their respective ability to
CC form physical interactions with the molecular interaction site. The
CC method also describes (1) RNA comprising a joined sequence of at least 24
CC nucleotides but not more than 70 nucleotides and having secondary
CC structure defined by: (a) 3 nucleotides forming a first side of a first
CC double stranded (ds) region; (b) 2 nucleotides forming a first side of an
CC internal loop region; (c) 4 nucleotides forming an end loop region; (e) 4
CC ds region; (d) 4 or 5 nucleotides forming a second side of the second ds region; (f) 4
CC nucleotides forming a second side of the internal loop region; and (g) 3
CC nucleotides forming a second side of the second ds region; (f) 4
CC nucleotides forming a second side of the internal loop region; and (g) 3
CC nucleotides forming a second side of the first ds region; (2) a purified
CC and isolated RNA fragment comprising the human sequence
CC UUUACACAUAUCUAGUACAGAAAAUC (II). The methods and products can be
CC used for identifying agents which modulate the activity of biomolecules,
CC particularly RNA. Such agents can be used as pharmaceutical, agricultural
CC or industrial compounds
XX
SQ Sequence 46 BP; 14 A; 7 C; 9 G; 16 T; 0 U; 0 Other;
Query Match 76.6%; Score 22.2; DB 3; Length 46;
Best Local Similarity 59.3%; Pred. No. 3.1;
Matches 16; Conservative 8; Mismatches 3; Indels 0; Gaps 0;
QY 2 AUGAUUUUUUUUUAAGCCUAGGGC 28
| | | | | | | | | | | | | | | | | | | |
Db 20 AAGATTCCTTTTGAAGCCCAAGGGC 46
| | | | | | | | | | | | | | | | | | | |
RESULT 36
AAA71105
ID AAA71090 standard; DNA; 46 BP.
XX
AC
XX AAA71105;
XX
DT 27-APR-2001 (first entry)
XX
DE Molecular interaction site RNA #191.
XX
KW Modulator; identification; molecular interaction; virtual library; ss.
XX
OS Unidentified.
XX
FN WO9958947-A2.
XX
PD 18-NOV-1999.
XX
PF 12-MAY-1999; 99WO-US010361.
XX
PR 12-MAY-1998; 98US-00076404.
XX
PR 12-MAY-1998; 98US-0085092P.
XX
PA (ISIS-) ISIS PHARM INC.
XX
XX Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;
PI Hofstadler S, Mcneil J;
XX
XX WPI; 2000-086439/07.
XX
XX Identifying compounds which modulate activity of target biomolecules,
PT used to provide compounds which can be used as pharmacological,
PT agricultural and industrial compounds.
XX
XX Example 7; Fig 122; 405pp; English.
XX
XX This invention describes a novel method for identifying compounds which
CC modulate the activity of a target biomolecule. The method uses 3-
CC dimensional representations of the biomolecule and a library of compounds
CC and comprises (a) identifying at least one molecular interaction site of
CC the target RNA; (b) generating in silico a virtual library of compounds
CC predicted or calculated to interact with the molecular interaction site;
CC and (c) comparing 3-dimensional (3-D) representations of the target RNA
CC with members of the virtual library of compounds to generate a hierarchy
CC of the compounds ranked in accordance with their respective ability to
CC form physical interactions with the molecular interaction site. The
CC method also describes (1) RNA comprising a joined sequence of at least 24
CC nucleotides but not more than 70 nucleotides and having secondary
CC structure defined by: (a) 3 nucleotides forming a first side of a first
CC double stranded (ds) region; (b) 2 nucleotides forming a first side of an
CC internal loop region; (c) 4 nucleotides forming an end loop region; (e) 4
CC ds region; (d) 4 or 5 nucleotides forming an end loop region; (f) 4
CC nucleotides forming a second side of the second ds region; (f) 4
CC nucleotides forming a second side of the internal loop region; and (g) 3
CC nucleotides forming a second side of the first ds region; (2) a purified
CC and isolated RNA fragment comprising the human sequence
CC UUUACACAUAUCUAGUACAGAAAAUC (II). The methods and products can be
CC used for identifying agents which modulate the activity of biomolecules,
CC particularly RNA. Such agents can be used as pharmaceutical, agricultural
CC or industrial compounds
XX
SQ Sequence 46 BP; 14 A; 7 C; 9 G; 16 T; 0 U; 0 Other;
Query Match 76.6%; Score 22.2; DB 3; Length 46;
Best Local Similarity 88.9%; Pred. No. 3.1;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 AUGAUUUUUUUUUAAGCCUAGGGC 28
| | | | | | | | | | | | | | | | | | | |
Db 20 AAGAUUUUUUUUUAAGCCCAAGGGC 46
| | | | | | | | | | | | | | | | | | | |
RESULT 37
AAA71090
ID AAA71090 standard; DNA; 46 BP.
```

```

XX AC AAA71090;
XX DT 27-APR-2001 (first entry)
XX DE Molecular interaction site DNA #113.
XX KW Modulator; identification; molecular interaction; virtual library; ss.
XX OS Unidentified.
XX PN WO9958947-A2.
XX PD 18-NOV-1999.
XX PF 12-MAY-1999; 99WO-US010361.
XX PR 12-MAY-1998; 98US-00076404.
XX PR 12-MAY-1998; 98US-0085092P.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;
XX PI Hofstadler S, Mcneil J;
XX DR WPI; 2000-086439/07.
XX PT Identifying compounds which modulate activity of target biomolecules,
XX PT used to provide compounds which can be used as pharmacological,
XX PT agricultural and industrial compounds.
XX PS Example 7; Fig 121; 405pp; English.
XX CC This invention describes a novel method for identifying compounds which
XX CC modulate the activity of a target biomolecule. The method uses 3-
XX CC dimensional representations of the biomolecule and a library of compounds
XX CC and comprises (a) identifying at least one molecular interaction site of
XX CC the target RNA; (b) generating in silico a virtual library of compounds
XX CC predicted or calculated to interact with the molecular interaction site;
XX CC and (c) comparing 3-dimensional (3-D) representations of the target RNA
XX CC with members of the virtual library of compounds to generate a hierarchy
XX CC of the compounds ranked in accordance with their respective ability to
XX CC form physical interactions with the molecular interaction site. The
XX CC method also describes (1) RNA comprising a joined sequence of at least 24
XX CC nucleotides but not more than 70 nucleotides and having secondary
XX CC structure defined by: (a) 3 nucleotides forming a first side of a first
XX CC internal loop region; (b) 2 nucleotides forming a first side of a second
XX CC double stranded (ds) region; (c) 4 nucleotides forming a first side of an
XX CC internal loop region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4
XX CC ds region; (f) 4 or 5 nucleotides forming a second side of a first
XX CC nucleotides forming a second side of the second ds region; and (g) 3
XX CC nucleotides forming a second side of the first ds region; (2) a purified
XX CC and isolated RNA fragment comprising the human sequence
XX CC UUUACACAAUUAUCUUAAGCCUAGGGGC (II). The methods and products can be
XX CC used for identifying agents which modulate the activity of biomolecules,
XX CC particularly RNA. Such agents can be used as pharmaceutical, agricultural
XX CC or industrial compounds
XX SQ Sequence 46 BP; 14 A; 7 C; 9 G; 16 T; 0 U; 0 Other;

Query Match 76.6%; Score 22.2; DB 3; Length 46;
Best Local Similarity 59.3%; Pred. No. 3.1;
Matches 16; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY 2 AUGAUUUUUUUUGAAGCCUAGGGGC 28
| | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | |
Db 20 AAGATTCTTTTGTAGCCCAAGGGC 46

RESULT 38
AAA71111
ID AAA71111 standard; RNA; 46 BP.
XX

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```

AC AAA71111;
XX DT 27-APR-2001 (first entry)
XX DE Molecular interaction site RNA #187.
XX KW Modulator; identification; molecular interaction; virtual library; ss.
XX OS Unidentified.
XX PN WO9958947-A2.
XX PD 18-NOV-1999.
XX PF 12-MAY-1999; 99WO-US010361.
XX PR 12-MAY-1998; 98US-00076404.
XX PR 12-MAY-1998; 98US-0085092P.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;
XX PI Hofstadler S, Mcneil J;
XX DR WPI; 2000-086439/07.
XX PT Identifying compounds which modulate activity of target biomolecules,
XX PT used to provide compounds which can be used as pharmacological,
XX PT agricultural and industrial compounds.
XX PS Example 7; Fig 122; 405pp; English.
XX CC This invention describes a novel method for identifying compounds which
XX CC modulate the activity of a target biomolecule. The method uses 3-
XX CC dimensional representations of the biomolecule and a library of compounds
XX CC and comprises (a) identifying at least one molecular interaction site of
XX CC the target RNA; (b) generating in silico a virtual library of compounds
XX CC predicted or calculated to interact with the molecular interaction site;
XX CC and (c) comparing 3-dimensional (3-D) representations of the target RNA
XX CC with members of the virtual library of compounds to generate a hierarchy
XX CC of the compounds ranked in accordance with their respective ability to
XX CC form physical interactions with the molecular interaction site. The
XX CC method also describes (1) RNA comprising a joined sequence of at least 24
XX CC nucleotides but not more than 70 nucleotides and having secondary
XX CC structure defined by: (a) 3 nucleotides forming a first side of a first
XX CC internal loop region; (b) 2 nucleotides forming a first side of a second
XX CC double stranded (ds) region; (c) 4 nucleotides forming a first side of an
XX CC internal loop region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4
XX CC ds region; (f) 4 or 5 nucleotides forming a second side of a first
XX CC nucleotides forming a second side of the second ds region; and (g) 3
XX CC nucleotides forming a second side of the first ds region; (2) a purified
XX CC and isolated RNA fragment comprising the human sequence
XX CC UUUACACAAUUAUCUUAAGCCUAGGGGC (II). The methods and products can be
XX CC used for identifying agents which modulate the activity of biomolecules,
XX CC particularly RNA. Such agents can be used as pharmaceutical, agricultural
XX CC or industrial compounds
XX SQ Sequence 46 BP; 9 A; 11 C; 9 G; 0 T; 17 U; 0 Other;

Query Match 74.5%; Score 21.6; DB 3; Length 46;
Best Local Similarity 85.7%; Pred. No. 5.7;
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 UUAUUAUUUUUUUGAAGCCUAGGGGC 28
| | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | |
Db 19 UUUUAUUUUUUUGAAGCCUAGGGGC 46

RESULT 39
AAA71095
ID AAA71095 standard; DNA; 46 BP.
XX
XX AAA71095;

```



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OM nucleic - nucleic search, using sw model

Run on: April 18, 2004, 08:41:44 ; Search time 159.667 Seconds  
(without alignments)  
812.711 Million cell updates/sec

Title: US-09-310-844C-23

Perfect score: 29

Sequence: 1 nmgaucaunungaaagccnangnm 29

Scoring table: IDENTITY\_NUC

Gapop 10.0, Gapext 1.0

Searched: 2890132 seqs, 223790429 residues

Total number of hits satisfying chosen parameters: 1657368

Minimum DB seq length: 0

Maximum DB seq length: 80

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications NA:

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2: /cgn2\_6/ptodata/1/pubna/PCT\_NEW\_PUB.seq:  
3: /cgn2\_6/ptodata/1/pubna/US06\_NEW\_PUB.seq:  
4: /cgn2\_6/ptodata/1/pubna/US06\_PUBCOMB.seq:  
5: /cgn2\_6/ptodata/1/pubna/US07\_NEW\_PUB.seq:  
6: /cgn2\_6/ptodata/1/pubna/PCTUS\_PUBCOMB.seq:  
7: /cgn2\_6/ptodata/1/pubna/US08\_NEW\_PUB.seq:  
8: /cgn2\_6/ptodata/1/pubna/US08\_PUBCOMB.seq:  
9: /cgn2\_6/ptodata/1/pubna/US09A\_PUBCOMB.seq:  
10: /cgn2\_6/ptodata/1/pubna/US09B\_PUBCOMB.seq:  
11: /cgn2\_6/ptodata/1/pubna/US09C\_PUBCOMB.seq:  
12: /cgn2\_6/ptodata/1/pubna/US09\_NEW\_PUB.seq:  
13: /cgn2\_6/ptodata/1/pubna/US10A\_PUBCOMB.seq:  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | ID                      | Description       |
|------------|-------|-------------|--------|-------------------------|-------------------|
| 1          | 12.8  | 44.1        | 30     | 12 US-10-335-977-10024  | Sequence 10024, A |
| 2          | 12.8  | 44.1        | 68     | 8 US-08-781-966A-2762   | Sequence 2762, Ap |
| 3          | 12.8  | 44.1        | 68     | 12 US-10-329-624-2762   | Sequence 2762, Ap |
| C 4        | 12.4  | 42.8        | 60     | 10 US-09-908-975-18725  | Sequence 18725, A |
| C 5        | 12.4  | 42.8        | 65     | 10 US-09-908-975-2848   | Sequence 2848, Ap |
| 6          | 12.2  | 42.1        | 50     | 15 US-10-131-827-454    | Sequence 454, App |
| 7          | 12.2  | 42.1        | 60     | 10 US-09-908-975-9828   | Sequence 9828, Ap |
| C 8        | 12.2  | 42.1        | 60     | 10 US-09-908-975-15109  | Sequence 15109, A |
| 9          | 12.2  | 42.1        | 60     | 10 US-09-908-975-18934  | Sequence 18934, A |
| 10         | 12.2  | 42.1        | 60     | 10 US-09-908-975-18934  | Sequence 18934, A |
| 11         | 11.8  | 40.7        | 25     | 14 US-10-098-263B-76444 | Sequence 76444, A |
| 12         | 11.8  | 40.7        | 47     | 9 US-09-230-926A-35     | Sequence 35, Appl |
| C 13       | 11.8  | 40.7        | 60     | 10 US-09-908-975-15914  | Sequence 15914, A |
| 14         | 11.8  | 40.7        | 60     | 10 US-09-908-975-17626  | Sequence 17626, A |
| 15         | 11.8  | 40.7        | 65     | 10 US-09-908-975-1254   | Sequence 1254, Ap |

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|----|----|-----------------------|--------------------|
| 65 | 10 | US-09-908-975-30297   | Sequence 30297, A  |
| 65 | 14 | US-10-032-585-316     | Sequence 316, App  |
| 77 | 9  | US-09-738-968-9       | Sequence 9, Appl   |
| 77 | 9  | US-09-738-968-10      | Sequence 10, Appl  |
| 24 | 10 | US-09-964-895-27      | Sequence 27, Appl  |
| 24 | 14 | US-10-058-152-26      | Sequence 26, Appl  |
| 31 | 10 | US-08-848-754A-6937   | Sequence 6937, Ap  |
| 31 | 10 | US-08-848-754A-7188   | Sequence 7188, Ap  |
| 31 | 10 | US-08-848-754A-7495   | Sequence 7495, Ap  |
| 31 | 10 | US-08-740-332-6639    | Sequence 6639, Ap  |
| 31 | 10 | US-08-740-332-9154    | Sequence 9154, Ap  |
| 31 | 10 | US-09-817-879-6639    | Sequence 6639, Ap  |
| 31 | 10 | US-09-817-879-9154    | Sequence 9154, Ap  |
| 31 | 14 | US-10-163-552-1019    | Sequence 1019, Ap  |
| 31 | 14 | US-10-156-306-3281    | Sequence 3281, Ap  |
| 36 | 9  | US-09-904-599A-7      | Sequence 7, Appl   |
| 38 | 15 | US-10-388-329-15      | Sequence 15, Appl  |
| 56 | 10 | US-09-800-130A-8      | Sequence 8, Appl   |
| 56 | 14 | US-10-413-909-8       | Sequence 8, Appl   |
| 60 | 10 | US-09-908-975-5781    | Sequence 5781, Ap  |
| 60 | 10 | US-09-908-975-12753   | Sequence 12753, A  |
| 60 | 10 | US-09-908-975-14781   | Sequence 14781, A  |
| 65 | 10 | US-09-908-975-24835   | Sequence 24835, A  |
| 65 | 10 | US-09-908-975-23918   | Sequence 23918, A  |
| 21 | 15 | US-10-435-696-379     | Sequence 279, App  |
| 25 | 14 | US-10-098-263B-5191   | Sequence 5191, Ap  |
| 25 | 14 | US-10-098-263B-5192   | Sequence 5192, Ap  |
| 25 | 14 | US-10-098-263B-94421  | Sequence 94421, A  |
| 44 | 14 | US-10-207-655-28      | Sequence 28, Appl  |
| 44 | 14 | US-10-053-530-28      | Sequence 28, Appl  |
| 60 | 10 | US-09-908-975-6202    | Sequence 6202, Ap  |
| 60 | 10 | US-09-908-975-7920    | Sequence 7920, Ap  |
| 60 | 10 | US-09-908-975-20533   | Sequence 20533, A  |
| 60 | 12 | US-10-296-734-206     | Sequence 206, App  |
| 65 | 10 | US-09-908-975-4740    | Sequence 4740, Ap  |
| 25 | 12 | US-10-150-407-28      | Sequence 28, Appl  |
| 25 | 14 | US-10-098-263B-37315  | Sequence 37315, A  |
| 25 | 14 | US-10-098-263B-37316  | Sequence 37316, A  |
| 25 | 14 | US-10-098-263B-100367 | Sequence 100367, A |
| 25 | 14 | US-10-098-263B-129996 | Sequence 129996, A |
| 25 | 15 | US-10-346-880-28      | Sequence 28, Appl  |
| 33 | 12 | US-10-150-407-29      | Sequence 29, Appl  |
| 33 | 15 | US-10-346-880-29      | Sequence 29, Appl  |
| 38 | 15 | US-10-424-233-66      | Sequence 66, Appl  |
| 41 | 14 | US-09-852-385-2       | Sequence 2, Appl   |
| 41 | 14 | US-10-005-956-212     | Sequence 212, App  |
| 47 | 15 | US-10-349-143-2842    | Sequence 2842, Ap  |
| 50 | 15 | US-10-131-827-3842    | Sequence 3842, Ap  |
| 50 | 15 | US-10-131-827-4871    | Sequence 4871, Ap  |
| 50 | 15 | US-10-131-827-6768    | Sequence 6768, Ap  |
| 50 | 15 | US-10-131-827-7158    | Sequence 7158, Ap  |
| 50 | 15 | US-10-131-827-7452    | Sequence 7452, Ap  |
| 50 | 15 | US-10-131-827-7531    | Sequence 7531, Ap  |
| 52 | 14 | US-10-139-662-6       | Sequence 6, Appl   |
| 52 | 14 | US-10-139-683-6       | Sequence 6, Appl   |
| 52 | 14 | US-10-143-618-6       | Sequence 6, Appl   |
| 60 | 10 | US-09-908-975-6077    | Sequence 6077, Ap  |
| 60 | 10 | US-09-908-975-15988   | Sequence 15988, A  |
| 60 | 10 | US-09-908-975-22254   | Sequence 22254, A  |
| 65 | 10 | US-09-908-975-3427    | Sequence 3427, Ap  |
| 65 | 10 | US-09-908-975-3925    | Sequence 3925, Ap  |
| 65 | 14 | US-10-032-585-2204    | Sequence 2204, Ap  |
| 69 | 14 | US-10-106-698-3906    | Sequence 3906, Ap  |
| 80 | 15 | US-10-448-250-78      | Sequence 78, Appl  |
| 17 | 10 | US-09-740-333-1228    | Sequence 1228, Ap  |
| 17 | 10 | US-09-740-333-3327    | Sequence 3327, Ap  |
| 17 | 10 | US-09-817-879-1428    | Sequence 1428, Ap  |
| 17 | 10 | US-09-817-879-3327    | Sequence 3327, Ap  |
| 30 | 9  | US-09-465-802-6       | Sequence 6, Appl   |
| 32 | 9  | US-09-810-506-10      | Sequence 10, Appl  |
| 34 | 15 | US-10-400-487-2       | Sequence 2, Appl   |
| 34 | 15 | US-10-400-487-5       | Sequence 5, Appl   |









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|-------|----|------|----|----|--------------------|--------------------|-------|----|------|----|----|-----------------------|--------------------|
| 527   | 10 | 34.5 | 22 | 14 | US-10-362-439-131  | Sequence 131, App  | 600   | 10 | 34.5 | 25 | 11 | US-09-908-576-321     | Sequence 321, App  |
| C 528 | 10 | 34.5 | 24 | 9  | US-09-962-537-49   | Sequence 49, Appl  | 601   | 10 | 34.5 | 25 | 12 | US-09-903-640-321     | Sequence 321, App  |
| C 529 | 10 | 34.5 | 24 | 9  | US-09-962-537-50   | Sequence 50, Appl  | 602   | 10 | 34.5 | 25 | 12 | US-09-908-093-321     | Sequence 321, App  |
| C 530 | 10 | 34.5 | 24 | 9  | US-09-962-537-51   | Sequence 51, Appl  | 603   | 10 | 34.5 | 25 | 12 | US-09-904-485-321     | Sequence 321, App  |
| C 531 | 10 | 34.5 | 24 | 9  | US-09-962-537-52   | Sequence 52, Appl  | 604   | 10 | 34.5 | 25 | 12 | US-09-905-348-321     | Sequence 321, App  |
| C 532 | 10 | 34.5 | 24 | 10 | US-09-940-185-233  | Sequence 233, App  | 605   | 10 | 34.5 | 25 | 12 | US-10-298-993-321     | Sequence 321, App  |
| C 533 | 10 | 34.5 | 24 | 14 | US-10-303-157-44   | Sequence 44, Appl  | 606   | 10 | 34.5 | 25 | 12 | US-10-448-933-321     | Sequence 321, App  |
| 534   | 10 | 34.5 | 25 | 9  | US-09-909-320-321  | Sequence 321, App  | 607   | 10 | 34.5 | 25 | 14 | US-10-098-263B-4855   | Sequence 4855, App |
| 535   | 10 | 34.5 | 25 | 9  | US-09-909-088B-321 | Sequence 321, App  | C 608 | 10 | 34.5 | 25 | 14 | US-10-098-263B-18785  | Sequence 18785, A  |
| 536   | 10 | 34.5 | 25 | 9  | US-09-905-291A-321 | Sequence 321, App  | C 609 | 10 | 34.5 | 25 | 14 | US-10-098-263B-18785  | Sequence 18785, A  |
| 537   | 10 | 34.5 | 25 | 9  | US-09-902-853-321  | Sequence 321, App  | C 610 | 10 | 34.5 | 25 | 14 | US-10-098-263B-26155  | Sequence 26155, A  |
| 538   | 10 | 34.5 | 25 | 9  | US-09-907-824-321  | Sequence 321, App  | C 611 | 10 | 34.5 | 25 | 14 | US-10-098-263B-33382  | Sequence 33382, A  |
| 539   | 10 | 34.5 | 25 | 9  | US-09-907-841-321  | Sequence 321, App  | C 612 | 10 | 34.5 | 25 | 14 | US-10-098-263B-33382  | Sequence 33382, A  |
| 540   | 10 | 34.5 | 25 | 10 | US-09-904-011-321  | Sequence 321, App  | C 613 | 10 | 34.5 | 25 | 14 | US-10-098-263B-35554  | Sequence 35554, A  |
| 541   | 10 | 34.5 | 25 | 10 | US-09-906-742-321  | Sequence 321, App  | C 614 | 10 | 34.5 | 25 | 14 | US-10-098-263B-41786  | Sequence 41786, A  |
| 542   | 10 | 34.5 | 25 | 10 | US-09-906-838-321  | Sequence 321, App  | C 615 | 10 | 34.5 | 25 | 14 | US-10-098-263B-41786  | Sequence 41786, A  |
| 543   | 10 | 34.5 | 25 | 10 | US-09-907-613-321  | Sequence 321, App  | C 616 | 10 | 34.5 | 25 | 14 | US-10-098-263B-74206  | Sequence 74206, A  |
| 544   | 10 | 34.5 | 25 | 10 | US-09-907-942-321  | Sequence 321, App  | C 617 | 10 | 34.5 | 25 | 14 | US-10-098-263B-74206  | Sequence 74206, A  |
| 545   | 10 | 34.5 | 25 | 10 | US-09-904-859-321  | Sequence 321, App  | C 618 | 10 | 34.5 | 25 | 14 | US-10-098-263B-76979  | Sequence 76979, A  |
| 546   | 10 | 34.5 | 25 | 10 | US-09-909-204-321  | Sequence 321, App  | C 619 | 10 | 34.5 | 25 | 14 | US-10-098-263B-86313  | Sequence 86313, A  |
| 547   | 10 | 34.5 | 25 | 10 | US-09-904-820-321  | Sequence 321, App  | C 620 | 10 | 34.5 | 25 | 14 | US-10-098-263B-87420  | Sequence 87420, A  |
| 548   | 10 | 34.5 | 25 | 10 | US-09-904-786-321  | Sequence 321, App  | C 621 | 10 | 34.5 | 25 | 14 | US-10-098-263B-94430  | Sequence 94430, A  |
| 549   | 10 | 34.5 | 25 | 10 | US-09-906-646-321  | Sequence 321, App  | C 622 | 10 | 34.5 | 25 | 14 | US-10-098-263B-96618  | Sequence 96618, A  |
| 550   | 10 | 34.5 | 25 | 10 | US-09-906-700-321  | Sequence 321, App  | C 623 | 10 | 34.5 | 25 | 14 | US-10-098-263B-102495 | Sequence 102495, A |
| 551   | 10 | 34.5 | 25 | 10 | US-09-903-786-321  | Sequence 321, App  | C 624 | 10 | 34.5 | 25 | 14 | US-10-098-263B-114959 | Sequence 114959, A |
| 552   | 10 | 34.5 | 25 | 10 | US-09-902-903-321  | Sequence 321, App  | C 625 | 10 | 34.5 | 25 | 14 | US-10-299-976-321     | Sequence 321, App  |
| 553   | 10 | 34.5 | 25 | 10 | US-09-903-749A-321 | Sequence 321, App  | C 626 | 10 | 34.5 | 25 | 14 | US-10-299-937-321     | Sequence 321, App  |
| 554   | 10 | 34.5 | 25 | 10 | US-09-904-119-321  | Sequence 321, App  | C 627 | 10 | 34.5 | 25 | 14 | US-10-449-656-321     | Sequence 321, App  |
| 555   | 10 | 34.5 | 25 | 10 | US-09-904-956-321  | Sequence 321, App  | C 628 | 10 | 34.5 | 25 | 15 | US-10-448-713-321     | Sequence 321, App  |
| 556   | 10 | 34.5 | 25 | 10 | US-09-902-736-321  | Sequence 321, App  | C 629 | 10 | 34.5 | 25 | 16 | US-10-425-447-321     | Sequence 321, App  |
| 557   | 10 | 34.5 | 25 | 10 | US-09-907-794-321  | Sequence 321, App  | C 630 | 10 | 34.5 | 26 | 14 | US-10-033-717-27      | Sequence 27, Appl  |
| 558   | 10 | 34.5 | 25 | 10 | US-09-903-943-321  | Sequence 321, App  | C 631 | 10 | 34.5 | 27 | 11 | US-09-823-936-33      | Sequence 33, Appl  |
| 559   | 10 | 34.5 | 25 | 10 | US-09-904-462-321  | Sequence 321, App  | C 632 | 10 | 34.5 | 27 | 11 | US-09-405-032-60      | Sequence 60, Appl  |
| 560   | 10 | 34.5 | 25 | 10 | US-09-907-925-321  | Sequence 321, App  | C 633 | 10 | 34.5 | 27 | 12 | US-10-128-510-10      | Sequence 10, Appl  |
| 561   | 10 | 34.5 | 25 | 10 | US-09-902-682-321  | Sequence 321, App  | C 634 | 10 | 34.5 | 27 | 12 | US-10-187-496A-42     | Sequence 42, Appl  |
| 562   | 10 | 34.5 | 25 | 10 | US-09-903-520-321  | Sequence 321, App  | C 635 | 10 | 34.5 | 27 | 13 | US-10-193-142-10      | Sequence 10, Appl  |
| 563   | 10 | 34.5 | 25 | 10 | US-09-905-056-321  | Sequence 321, App  | C 636 | 10 | 34.5 | 27 | 14 | US-10-134-493-10      | Sequence 10, Appl  |
| 564   | 10 | 34.5 | 25 | 10 | US-09-909-064-321  | Sequence 321, App  | C 637 | 10 | 34.5 | 27 | 14 | US-10-112-892-16      | Sequence 16, Appl  |
| 565   | 10 | 34.5 | 25 | 10 | US-09-904-553-321  | Sequence 321, App  | C 638 | 10 | 34.5 | 27 | 14 | US-10-061-216-10      | Sequence 10, Appl  |
| 566   | 10 | 34.5 | 25 | 10 | US-09-905-381-321  | Sequence 321, App  | C 639 | 10 | 34.5 | 27 | 14 | US-10-286-140-33      | Sequence 33, Appl  |
| 567   | 10 | 34.5 | 25 | 10 | US-09-905-088-321  | Sequence 321, App  | C 640 | 10 | 34.5 | 27 | 15 | US-10-245-237B-53     | Sequence 53, Appl  |
| 568   | 10 | 34.5 | 25 | 10 | US-09-907-575-321  | Sequence 321, App  | C 641 | 10 | 34.5 | 28 | 10 | US-09-281-495-57      | Sequence 57, Appl  |
| 569   | 10 | 34.5 | 25 | 10 | US-09-905-075-321  | Sequence 321, App  | C 642 | 10 | 34.5 | 28 | 14 | US-10-272-206-39      | Sequence 29, Appl  |
| 570   | 10 | 34.5 | 25 | 10 | US-09-902-759-321  | Sequence 321, App  | C 643 | 10 | 34.5 | 28 | 14 | US-10-272-206-39      | Sequence 30, Appl  |
| 571   | 10 | 34.5 | 25 | 10 | US-09-902-634-321  | Sequence 321, App  | C 644 | 10 | 34.5 | 29 | 8  | US-08-834-666A-34     | Sequence 34, Appl  |
| 572   | 10 | 34.5 | 25 | 10 | US-09-902-713-321  | Sequence 321, App  | C 645 | 10 | 34.5 | 29 | 14 | US-10-122-013-2       | Sequence 2, Appl   |
| 573   | 10 | 34.5 | 25 | 10 | US-09-907-979-321  | Sequence 321, App  | C 646 | 10 | 34.5 | 30 | 9  | US-09-918-421-2       | Sequence 2, Appl   |
| 574   | 10 | 34.5 | 25 | 10 | US-09-902-615-321  | Sequence 321, App  | C 647 | 10 | 34.5 | 30 | 14 | US-10-166-225A-121    | Sequence 121, App  |
| 575   | 10 | 34.5 | 25 | 10 | US-09-903-925-321  | Sequence 321, App  | C 648 | 10 | 34.5 | 31 | 9  | US-09-801-274-422     | Sequence 422, App  |
| 576   | 10 | 34.5 | 25 | 10 | US-09-940-185-4214 | Sequence 4214, App | C 649 | 10 | 34.5 | 31 | 9  | US-09-928-457-48      | Sequence 48, Appl  |
| 577   | 10 | 34.5 | 25 | 10 | US-09-906-760A-321 | Sequence 321, App  | C 650 | 10 | 34.5 | 31 | 9  | US-09-864-785-2376    | Sequence 2376, App |
| 578   | 10 | 34.5 | 25 | 10 | US-09-903-823-321  | Sequence 321, App  | C 651 | 10 | 34.5 | 31 | 9  | US-09-864-785-2347    | Sequence 2347, App |
| 579   | 10 | 34.5 | 25 | 10 | US-09-907-652-321  | Sequence 321, App  | C 652 | 10 | 34.5 | 31 | 9  | US-09-864-785-2338    | Sequence 2338, App |
| 580   | 10 | 34.5 | 25 | 10 | US-09-902-572A-321 | Sequence 321, App  | C 653 | 10 | 34.5 | 31 | 9  | US-09-864-785-2555    | Sequence 2555, App |
| 581   | 10 | 34.5 | 25 | 10 | US-09-902-979-321  | Sequence 321, App  | C 654 | 10 | 34.5 | 31 | 10 | US-09-730-289B-3190   | Sequence 3190, App |
| 582   | 10 | 34.5 | 25 | 10 | US-09-905-125-321  | Sequence 321, App  | C 655 | 10 | 34.5 | 31 | 10 | US-09-730-289B-3259   | Sequence 3259, App |
| 583   | 10 | 34.5 | 25 | 10 | US-09-906-815A-321 | Sequence 321, App  | C 656 | 10 | 34.5 | 31 | 10 | US-09-780-533A-5242   | Sequence 5242, App |
| 584   | 10 | 34.5 | 25 | 10 | US-09-905-449-321  | Sequence 321, App  | C 657 | 10 | 34.5 | 31 | 10 | US-09-780-533A-5317   | Sequence 5317, App |
| 585   | 10 | 34.5 | 25 | 10 | US-09-903-806-321  | Sequence 321, App  | C 658 | 10 | 34.5 | 31 | 10 | US-09-780-533A-5402   | Sequence 5402, App |
| 586   | 10 | 34.5 | 25 | 10 | US-09-904-932-321  | Sequence 321, App  | C 659 | 10 | 34.5 | 31 | 10 | US-09-780-533A-5515   | Sequence 5515, App |
| 587   | 10 | 34.5 | 25 | 10 | US-09-904-838-321  | Sequence 321, App  | C 660 | 10 | 34.5 | 31 | 10 | US-09-780-533A-5526   | Sequence 5526, App |
| 588   | 10 | 34.5 | 25 | 10 | US-09-906-777-321  | Sequence 321, App  | C 661 | 10 | 34.5 | 31 | 10 | US-09-780-533A-5638   | Sequence 5638, App |
| 589   | 10 | 34.5 | 25 | 10 | US-09-903-603A-321 | Sequence 321, App  | C 662 | 10 | 34.5 | 31 | 10 | US-09-877-478-4853    | Sequence 4853, App |
| 590   | 10 | 34.5 | 25 | 10 | US-09-904-532-321  | Sequence 321, App  | C 663 | 10 | 34.5 | 31 | 10 | US-09-877-478-4863    | Sequence 4863, App |
| 591   | 10 | 34.5 | 25 | 10 | US-09-904-766-591  | Sequence 321, App  | C 664 | 10 | 34.5 | 31 | 10 | US-09-877-478-5046    | Sequence 5046, App |
| 592   | 10 | 34.5 | 25 | 10 | US-09-904-920A-321 | Sequence 321, App  | C 665 | 10 | 34.5 | 31 | 10 | US-09-848-754A-6664   | Sequence 6664, App |
| 593   | 10 | 34.5 | 25 | 10 | US-09-904-877A-321 | Sequence 321, App  | C 666 | 10 | 34.5 | 31 | 10 | US-09-848-754A-6683   | Sequence 6683, App |
| 594   | 10 | 34.5 | 25 | 10 | US-09-903-562-321  | Sequence 321, App  | C 667 | 10 | 34.5 | 31 | 10 | US-09-848-754A-6756   | Sequence 6756, App |
| 595   | 10 | 34.5 | 25 | 10 | US-09-906-618-321  | Sequence 321, App  | C 668 | 10 | 34.5 | 31 | 10 | US-09-848-754A-6794   | Sequence 6794, App |
| 596   | 10 | 34.5 | 25 | 10 | US-09-907-728-321  | Sequence 321, App  | C 669 | 10 | 34.5 | 31 | 10 | US-09-848-754A-6920   | Sequence 6920, App |
| 597   | 10 | 34.5 | 25 | 11 | US-09-904-805-321  | Sequence 321, App  | C 670 | 10 | 34.5 | 31 | 10 | US-09-848-754A-6940   | Sequence 6940, App |
| 598   | 10 | 34.5 | 25 | 11 | US-09-904-938A-321 | Sequence 321, App  | C 671 | 10 | 34.5 | 31 | 10 | US-09-848-754A-6940   | Sequence 6940, App |
| 599   | 10 | 34.5 | 25 | 11 | US-09-906-722A-321 | Sequence 321, App  | C 672 | 10 | 34.5 | 31 | 10 | US-09-848-754A-6978   | Sequence 6978, App |



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| C 673 | 10 | 34.5 | 31 | 10 | US-09-848-754A-7074 | Sequence 7074, Ap | C 746 | 10 | 34.5 | 31 | 10 | US-09-817-879-6200 | Sequence 6200, Ap |
| C 674 | 10 | 34.5 | 31 | 10 | US-09-848-754A-7134 | Sequence 7134, Ap | C 747 | 10 | 34.5 | 31 | 10 | US-09-817-879-6262 | Sequence 6262, Ap |
| C 675 | 10 | 34.5 | 31 | 10 | US-09-848-754A-7261 | Sequence 7261, Ap | C 748 | 10 | 34.5 | 31 | 10 | US-09-817-879-6309 | Sequence 6309, Ap |
| C 676 | 10 | 34.5 | 31 | 10 | US-09-848-754A-7336 | Sequence 7336, Ap | C 749 | 10 | 34.5 | 31 | 10 | US-09-817-879-6330 | Sequence 6330, Ap |
| C 677 | 10 | 34.5 | 31 | 10 | US-09-776-474-2365  | Sequence 2365, Ap | C 750 | 10 | 34.5 | 31 | 10 | US-09-817-879-6830 | Sequence 6830, Ap |
| C 678 | 10 | 34.5 | 31 | 10 | US-09-776-474-2391  | Sequence 2391, Ap | C 751 | 10 | 34.5 | 31 | 10 | US-09-817-879-6847 | Sequence 6847, Ap |
| C 679 | 10 | 34.5 | 31 | 10 | US-09-776-474-2400  | Sequence 2400, Ap | C 752 | 10 | 34.5 | 31 | 10 | US-09-817-879-6961 | Sequence 6961, Ap |
| C 680 | 10 | 34.5 | 31 | 10 | US-09-930-423-3350  | Sequence 3350, Ap | C 753 | 10 | 34.5 | 31 | 10 | US-09-817-879-6972 | Sequence 6972, Ap |
| C 681 | 10 | 34.5 | 31 | 10 | US-09-930-423-3522  | Sequence 3522, Ap | C 754 | 10 | 34.5 | 31 | 10 | US-09-817-879-7002 | Sequence 7002, Ap |
| C 682 | 10 | 34.5 | 31 | 10 | US-09-930-423-3523  | Sequence 3523, Ap | C 755 | 10 | 34.5 | 31 | 10 | US-09-817-879-7066 | Sequence 7066, Ap |
| C 683 | 10 | 34.5 | 31 | 10 | US-09-930-423-3530  | Sequence 3530, Ap | C 756 | 10 | 34.5 | 31 | 10 | US-09-817-879-7097 | Sequence 7097, Ap |
| C 684 | 10 | 34.5 | 31 | 10 | US-09-930-423-3558  | Sequence 3558, Ap | C 757 | 10 | 34.5 | 31 | 10 | US-09-817-879-7114 | Sequence 7114, Ap |
| C 685 | 10 | 34.5 | 31 | 10 | US-09-930-423-3636  | Sequence 3636, Ap | C 758 | 10 | 34.5 | 31 | 10 | US-09-817-879-7218 | Sequence 7218, Ap |
| C 686 | 10 | 34.5 | 31 | 10 | US-09-780-154-1973  | Sequence 1973, Ap | C 759 | 10 | 34.5 | 31 | 10 | US-09-817-879-7276 | Sequence 7276, Ap |
| C 687 | 10 | 34.5 | 31 | 10 | US-08-827-385A-2088 | Sequence 2088, Ap | C 760 | 10 | 34.5 | 31 | 10 | US-09-817-879-7877 | Sequence 7877, Ap |
| C 688 | 10 | 34.5 | 31 | 10 | US-09-827-395A-2139 | Sequence 2139, Ap | C 761 | 10 | 34.5 | 31 | 10 | US-09-817-879-7922 | Sequence 7922, Ap |
| C 689 | 10 | 34.5 | 31 | 10 | US-09-827-395A-2146 | Sequence 2146, Ap | C 762 | 10 | 34.5 | 31 | 10 | US-09-817-879-8270 | Sequence 8270, Ap |
| C 690 | 10 | 34.5 | 31 | 10 | US-09-740-332-4873  | Sequence 4873, Ap | C 763 | 10 | 34.5 | 31 | 10 | US-09-817-879-8509 | Sequence 8509, Ap |
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| C 692 | 10 | 34.5 | 31 | 10 | US-09-740-332-5272  | Sequence 5272, Ap | C 765 | 10 | 34.5 | 31 | 10 | US-09-817-879-8595 | Sequence 8595, Ap |
| C 693 | 10 | 34.5 | 31 | 10 | US-09-740-332-5363  | Sequence 5363, Ap | C 766 | 10 | 34.5 | 31 | 10 | US-09-817-879-8622 | Sequence 8622, Ap |
| C 694 | 10 | 34.5 | 31 | 10 | US-09-740-332-5394  | Sequence 5394, Ap | C 767 | 10 | 34.5 | 31 | 10 | US-09-817-879-8641 | Sequence 8641, Ap |
| C 695 | 10 | 34.5 | 31 | 10 | US-09-740-332-5437  | Sequence 5437, Ap | C 768 | 10 | 34.5 | 31 | 10 | US-09-817-879-8659 | Sequence 8659, Ap |
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| C 698 | 10 | 34.5 | 31 | 10 | US-09-740-332-6200  | Sequence 6200, Ap | C 771 | 10 | 34.5 | 31 | 10 | US-09-817-879-9111 | Sequence 9111, Ap |
| C 699 | 10 | 34.5 | 31 | 10 | US-09-740-332-6262  | Sequence 6262, Ap | C 772 | 10 | 34.5 | 31 | 10 | US-09-817-879-9156 | Sequence 9156, Ap |
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| C 701 | 10 | 34.5 | 31 | 10 | US-09-740-332-6630  | Sequence 6630, Ap | C 774 | 10 | 34.5 | 31 | 10 | US-09-817-879-9219 | Sequence 9219, Ap |
| C 702 | 10 | 34.5 | 31 | 10 | US-09-740-332-6847  | Sequence 6847, Ap | C 775 | 10 | 34.5 | 31 | 10 | US-09-817-879-9228 | Sequence 9228, Ap |
| C 703 | 10 | 34.5 | 31 | 10 | US-09-740-332-6961  | Sequence 6961, Ap | C 776 | 10 | 34.5 | 31 | 10 | US-09-817-879-9288 | Sequence 9288, Ap |
| C 704 | 10 | 34.5 | 31 | 10 | US-09-740-332-6972  | Sequence 6972, Ap | C 777 | 10 | 34.5 | 31 | 12 | US-10-342-902-4853 | Sequence 4853, Ap |
| C 705 | 10 | 34.5 | 31 | 10 | US-09-740-332-7002  | Sequence 7002, Ap | C 778 | 10 | 34.5 | 31 | 12 | US-10-342-902-4863 | Sequence 4863, Ap |
| C 706 | 10 | 34.5 | 31 | 10 | US-09-740-332-7066  | Sequence 7066, Ap | C 779 | 10 | 34.5 | 31 | 12 | US-09-927-045-3962 | Sequence 3962, Ap |
| C 707 | 10 | 34.5 | 31 | 10 | US-09-740-332-7097  | Sequence 7097, Ap | C 780 | 10 | 34.5 | 31 | 12 | US-09-927-045-4546 | Sequence 4546, Ap |
| C 708 | 10 | 34.5 | 31 | 10 | US-09-740-332-7114  | Sequence 7114, Ap | C 781 | 10 | 34.5 | 31 | 12 | US-09-927-045-4589 | Sequence 4589, Ap |
| C 709 | 10 | 34.5 | 31 | 10 | US-09-740-332-7218  | Sequence 7218, Ap | C 782 | 10 | 34.5 | 31 | 12 | US-10-430-882-2139 | Sequence 2139, Ap |
| C 710 | 10 | 34.5 | 31 | 10 | US-09-740-332-7276  | Sequence 7276, Ap | C 783 | 10 | 34.5 | 31 | 12 | US-10-430-882-2146 | Sequence 2146, Ap |
| C 711 | 10 | 34.5 | 31 | 10 | US-09-740-332-7809  | Sequence 7809, Ap | C 784 | 10 | 34.5 | 31 | 14 | US-10-163-552-1037 | Sequence 1037, Ap |
| C 712 | 10 | 34.5 | 31 | 10 | US-09-740-332-7877  | Sequence 7877, Ap | C 785 | 10 | 34.5 | 31 | 14 | US-10-163-552-1082 | Sequence 1082, Ap |
| C 713 | 10 | 34.5 | 31 | 10 | US-09-740-332-7922  | Sequence 7922, Ap | C 786 | 10 | 34.5 | 31 | 14 | US-10-163-552-1143 | Sequence 1143, Ap |
| C 714 | 10 | 34.5 | 31 | 10 | US-09-740-332-8270  | Sequence 8270, Ap | C 787 | 10 | 34.5 | 31 | 14 | US-10-163-552-1189 | Sequence 1189, Ap |
| C 715 | 10 | 34.5 | 31 | 10 | US-09-740-332-8509  | Sequence 8509, Ap | C 788 | 10 | 34.5 | 31 | 14 | US-10-163-552-1259 | Sequence 1259, Ap |
| C 716 | 10 | 34.5 | 31 | 10 | US-09-740-332-8556  | Sequence 8556, Ap | C 789 | 10 | 34.5 | 31 | 14 | US-10-163-552-1407 | Sequence 1407, Ap |
| C 717 | 10 | 34.5 | 31 | 10 | US-09-740-332-8595  | Sequence 8595, Ap | C 790 | 10 | 34.5 | 31 | 14 | US-10-163-552-1484 | Sequence 1484, Ap |
| C 718 | 10 | 34.5 | 31 | 10 | US-09-740-332-8622  | Sequence 8622, Ap | C 791 | 10 | 34.5 | 31 | 14 | US-10-163-552-1614 | Sequence 1614, Ap |
| C 719 | 10 | 34.5 | 31 | 10 | US-09-740-332-8641  | Sequence 8641, Ap | C 792 | 10 | 34.5 | 31 | 14 | US-10-163-552-1650 | Sequence 1650, Ap |
| C 720 | 10 | 34.5 | 31 | 10 | US-09-740-332-8659  | Sequence 8659, Ap | C 793 | 10 | 34.5 | 31 | 14 | US-10-163-552-1655 | Sequence 1655, Ap |
| C 721 | 10 | 34.5 | 31 | 10 | US-09-740-332-8853  | Sequence 8853, Ap | C 794 | 10 | 34.5 | 31 | 14 | US-10-163-552-1849 | Sequence 1849, Ap |
| C 722 | 10 | 34.5 | 31 | 10 | US-09-740-332-8862  | Sequence 8862, Ap | C 795 | 10 | 34.5 | 31 | 14 | US-10-163-552-1868 | Sequence 1868, Ap |
| C 723 | 10 | 34.5 | 31 | 10 | US-09-740-332-9084  | Sequence 9084, Ap | C 796 | 10 | 34.5 | 31 | 14 | US-10-163-552-1877 | Sequence 1877, Ap |
| C 724 | 10 | 34.5 | 31 | 10 | US-09-740-332-9111  | Sequence 9111, Ap | C 797 | 10 | 34.5 | 31 | 14 | US-10-163-552-1886 | Sequence 1886, Ap |
| C 725 | 10 | 34.5 | 31 | 10 | US-09-740-332-9156  | Sequence 9156, Ap | C 798 | 10 | 34.5 | 31 | 14 | US-10-156-306-2923 | Sequence 3283, Ap |
| C 726 | 10 | 34.5 | 31 | 10 | US-09-740-332-9207  | Sequence 9207, Ap | C 799 | 10 | 34.5 | 31 | 14 | US-10-156-306-3070 | Sequence 6409, Ap |
| C 727 | 10 | 34.5 | 31 | 10 | US-09-740-332-9219  | Sequence 9219, Ap | C 800 | 10 | 34.5 | 31 | 14 | US-10-156-306-6436 | Sequence 6426, Ap |
| C 728 | 10 | 34.5 | 31 | 10 | US-09-740-332-9228  | Sequence 9228, Ap | C 801 | 10 | 34.5 | 31 | 14 | US-10-156-306-6442 | Sequence 6435, Ap |
| C 729 | 10 | 34.5 | 31 | 10 | US-09-792-818-1600  | Sequence 1600, Ap | C 802 | 10 | 34.5 | 31 | 14 | US-10-156-306-6448 | Sequence 6442, Ap |
| C 730 | 10 | 34.5 | 31 | 10 | US-09-792-818-1672  | Sequence 1672, Ap | C 803 | 10 | 34.5 | 31 | 14 | US-10-156-306-6452 | Sequence 6448, Ap |
| C 731 | 10 | 34.5 | 31 | 10 | US-09-792-818-1770  | Sequence 1770, Ap | C 804 | 10 | 34.5 | 31 | 14 | US-10-156-306-6458 | Sequence 6452, Ap |
| C 732 | 10 | 34.5 | 31 | 10 | US-09-745-237A-3350 | Sequence 3350, Ap | C 805 | 10 | 34.5 | 31 | 14 | US-10-156-306-6464 | Sequence 6458, Ap |
| C 733 | 10 | 34.5 | 31 | 10 | US-09-745-237A-3522 | Sequence 3522, Ap | C 806 | 10 | 34.5 | 31 | 14 | US-10-156-306-6484 | Sequence 6484, Ap |
| C 734 | 10 | 34.5 | 31 | 10 | US-09-745-237A-3523 | Sequence 3523, Ap | C 807 | 10 | 34.5 | 31 | 14 | US-10-156-306-6488 | Sequence 6488, Ap |
| C 735 | 10 | 34.5 | 31 | 10 | US-09-745-237A-3530 | Sequence 3530, Ap | C 808 | 10 | 34.5 | 31 | 14 | US-10-156-306-6496 | Sequence 6496, Ap |
| C 736 | 10 | 34.5 | 31 | 10 | US-09-745-237A-3558 | Sequence 3558, Ap | C 809 | 10 | 34.5 | 31 | 14 | US-10-156-306-6511 | Sequence 6511, Ap |
| C 737 | 10 | 34.5 | 31 | 10 | US-09-817-879-4873  | Sequence 4873, Ap | C 810 | 10 | 34.5 | 31 | 14 | US-10-156-306-6521 | Sequence 6521, Ap |
| C 738 | 10 | 34.5 | 31 | 10 | US-09-817-879-4873  | Sequence 4873, Ap | C 811 | 10 | 34.5 | 31 | 14 | US-10-156-306-6535 | Sequence 6535, Ap |
| C 739 | 10 | 34.5 | 31 | 10 | US-09-817-879-5006  | Sequence 5006, Ap | C 812 | 10 | 34.5 | 31 | 14 | US-10-156-306-6541 | Sequence 6541, Ap |
| C 740 | 10 | 34.5 | 31 | 10 | US-09-817-879-5272  | Sequence 5272, Ap | C 813 | 10 | 34.5 | 31 | 14 | US-10-156-306-6542 | Sequence 6542, Ap |
| C 741 | 10 | 34.5 | 31 | 10 | US-09-817-879-5363  | Sequence 5363, Ap | C 814 | 10 | 34.5 | 31 | 14 | US-10-156-306-6548 | Sequence 6548, Ap |
| C 742 | 10 | 34.5 | 31 | 10 | US-09-817-879-5394  | Sequence 5394, Ap | C 815 | 10 | 34.5 | 31 | 14 | US-10-156-306-6552 | Sequence 6552, Ap |
| C 743 | 10 | 34.5 | 31 | 10 | US-09-817-879-5437  | Sequence 5437, Ap | C 816 | 10 | 34.5 | 31 | 14 | US-10-156-306-6558 | Sequence 6558, Ap |
| C 744 | 10 | 34.5 | 31 | 10 | US-09-817-879-5804  | Sequence 5804, Ap | C 817 | 10 | 34.5 | 31 | 14 | US-10-156-306-6721 | Sequence 6721, Ap |
| C 745 | 10 | 34.5 | 31 | 10 | US-09-817-879-5871  | Sequence 5871, Ap | C 818 | 10 | 34.5 | 31 | 14 | US-10-156-306-6736 | Sequence 6736, Ap |

|       |    |      |    |    |                      |                   |     |    |      |    |    |                      |                   |
|-------|----|------|----|----|----------------------|-------------------|-----|----|------|----|----|----------------------|-------------------|
| C 819 | 10 | 34.5 | 31 | 14 | US-10-238-700-1714   | Sequence 1714, Ap | 892 | 10 | 34.5 | 61 | 15 | US-10-437-169-66     | Sequence 66, Appl |
| C 820 | 10 | 34.5 | 31 | 14 | US-10-238-700-2415   | Sequence 2415, Ap | 893 | 10 | 34.5 | 63 | 12 | US-10-027-632-176912 | Sequence 176912,  |
| C 821 | 10 | 34.5 | 31 | 14 | US-10-238-700-3677   | Sequence 3677, Ap | 894 | 10 | 34.5 | 63 | 15 | US-10-027-632-176912 | Sequence 176912,  |
| C 822 | 10 | 34.5 | 31 | 14 | US-10-238-700-3777   | Sequence 3777, Ap | 895 | 10 | 34.5 | 65 | 10 | US-09-908-975-156    | Sequence 156, App |
| C 823 | 10 | 34.5 | 31 | 14 | US-10-238-700-3777   | Sequence 3777, Ap | 896 | 10 | 34.5 | 65 | 10 | US-09-908-975-2136   | Sequence 2136, Ap |
| C 824 | 10 | 34.5 | 31 | 14 | US-10-238-700-3845   | Sequence 3845, Ap | 897 | 10 | 34.5 | 65 | 10 | US-09-908-975-2596   | Sequence 2596, Ap |
| C 825 | 10 | 34.5 | 31 | 14 | US-10-238-700-3965   | Sequence 3965, Ap | 898 | 10 | 34.5 | 65 | 10 | US-09-908-975-3442   | Sequence 3442, Ap |
| C 826 | 10 | 34.5 | 31 | 14 | US-10-238-700-3967   | Sequence 3967, Ap | 899 | 10 | 34.5 | 65 | 10 | US-09-908-975-4004   | Sequence 4004, Ap |
| C 827 | 10 | 34.5 | 31 | 14 | US-10-238-700-4089   | Sequence 4089, Ap | 900 | 10 | 34.5 | 65 | 10 | US-09-908-975-2390   | Sequence 2390, Ap |
| C 828 | 10 | 34.5 | 31 | 14 | US-10-238-700-4435   | Sequence 4435, Ap | 901 | 10 | 34.5 | 65 | 10 | US-09-908-975-2390   | Sequence 2390, Ap |
| C 829 | 10 | 34.5 | 31 | 14 | US-10-238-700-4541   | Sequence 4541, Ap | 902 | 10 | 34.5 | 65 | 10 | US-09-908-975-25500  | Sequence 25500, A |
| C 830 | 10 | 34.5 | 31 | 14 | US-10-238-700-4552   | Sequence 4552, Ap | 903 | 10 | 34.5 | 65 | 10 | US-09-908-975-25539  | Sequence 25539, A |
| C 831 | 10 | 34.5 | 31 | 14 | US-10-230-006-1725   | Sequence 1725, Ap | 904 | 10 | 34.5 | 65 | 10 | US-09-908-975-26289  | Sequence 26289, A |
| C 832 | 10 | 34.5 | 31 | 14 | US-10-230-006-1740   | Sequence 1740, Ap | 905 | 10 | 34.5 | 65 | 10 | US-09-908-975-26414  | Sequence 26414, A |
| C 833 | 10 | 34.5 | 31 | 14 | US-10-230-006-1767   | Sequence 1767, Ap | 906 | 10 | 34.5 | 65 | 10 | US-09-908-975-27440  | Sequence 27440, A |
| C 834 | 10 | 34.5 | 31 | 14 | US-10-230-006-1949   | Sequence 1949, Ap | 907 | 10 | 34.5 | 65 | 10 | US-09-908-975-27529  | Sequence 27529, A |
| C 835 | 10 | 34.5 | 31 | 14 | US-10-230-006-1972   | Sequence 1972, Ap | 908 | 10 | 34.5 | 65 | 10 | US-09-908-975-28083  | Sequence 28083, A |
| C 836 | 10 | 34.5 | 31 | 14 | US-10-230-006-2011   | Sequence 2011, Ap | 909 | 10 | 34.5 | 65 | 10 | US-09-908-975-29336  | Sequence 29336, A |
| C 837 | 10 | 34.5 | 33 | 9  | US-09-784-508-7      | Sequence 7, Appli | 910 | 10 | 34.5 | 65 | 10 | US-09-908-975-29424  | Sequence 29424, A |
| C 838 | 10 | 34.5 | 33 | 14 | US-10-389-177-7      | Sequence 56, Appl | 911 | 10 | 34.5 | 65 | 10 | US-09-908-975-30118  | Sequence 30118, A |
| C 839 | 10 | 34.5 | 33 | 15 | US-10-360-828-56     | Sequence 56, Appl | 912 | 10 | 34.5 | 65 | 14 | US-10-313-542-258    | Sequence 258, App |
| C 840 | 10 | 34.5 | 35 | 10 | US-09-365-940-19     | Sequence 19, Appl | 913 | 10 | 34.5 | 65 | 14 | US-10-032-585-136    | Sequence 136, App |
| C 841 | 10 | 34.5 | 35 | 14 | US-10-200-242-19     | Sequence 19, Appl | 914 | 10 | 34.5 | 65 | 14 | US-10-032-585-433    | Sequence 433, App |
| C 842 | 10 | 34.5 | 35 | 15 | US-10-147-603-53     | Sequence 53, Appl | 915 | 10 | 34.5 | 65 | 14 | US-10-032-585-463    | Sequence 463, App |
| C 843 | 10 | 34.5 | 35 | 15 | US-10-200-242-19     | Sequence 19, Appl | 916 | 10 | 34.5 | 65 | 14 | US-10-032-585-3405   | Sequence 3405, Ap |
| C 844 | 10 | 34.5 | 35 | 15 | US-10-420-194-658    | Sequence 658, App | 917 | 10 | 34.5 | 72 | 14 | US-10-204-884-131    | Sequence 131, App |
| C 845 | 10 | 34.5 | 37 | 9  | US-09-924-154-9      | Sequence 9, Appli | 918 | 10 | 34.5 | 72 | 14 | US-10-029-386-15365  | Sequence 15365, A |
| C 846 | 10 | 34.5 | 38 | 11 | US-09-405-032-66     | Sequence 66, Appl | 919 | 10 | 34.5 | 80 | 14 | US-10-029-386-14002  | Sequence 14002, A |
| C 847 | 10 | 34.5 | 39 | 9  | US-09-894-633A-39    | Sequence 39, Appl | 920 | 10 | 34.5 | 80 | 15 | US-10-448-250-21     | Sequence 21, Appl |
| C 848 | 10 | 34.5 | 40 | 15 | US-10-411-066-121    | Sequence 121, App | 921 | 10 | 34.5 | 17 | 9  | US-09-866-108-10208  | Sequence 10208, A |
| C 849 | 10 | 34.5 | 41 | 12 | US-10-453-827-999    | Sequence 99, Appl | 922 | 10 | 33.8 | 17 | 9  | US-09-866-108-10209  | Sequence 10209, A |
| C 850 | 10 | 34.5 | 41 | 12 | US-10-339-674-46     | Sequence 46, Appl | 923 | 10 | 33.8 | 17 | 9  | US-09-827-998-281    | Sequence 281, App |
| C 851 | 10 | 34.5 | 41 | 12 | US-10-339-674-47     | Sequence 47, Appl | 924 | 10 | 33.8 | 17 | 9  | US-09-827-998-282    | Sequence 282, App |
| C 852 | 10 | 34.5 | 42 | 13 | US-10-339-674-45     | Sequence 45, Appl | 925 | 10 | 33.8 | 17 | 9  | US-09-827-998-283    | Sequence 283, App |
| C 853 | 10 | 34.5 | 42 | 13 | US-10-025-367-15     | Sequence 15, Appl | 926 | 10 | 33.8 | 17 | 9  | US-09-969-373-4322   | Sequence 4322, Ap |
| C 854 | 10 | 34.5 | 42 | 14 | US-10-186-867-16     | Sequence 16, Appl | 927 | 10 | 33.8 | 17 | 10 | US-09-877-478-163    | Sequence 163, App |
| C 855 | 10 | 34.5 | 42 | 14 | US-10-400-377-39     | Sequence 39, Appl | 928 | 10 | 33.8 | 17 | 10 | US-09-877-478-1470   | Sequence 1470, Ap |
| C 856 | 10 | 34.5 | 42 | 14 | US-10-400-708-39     | Sequence 39, Appl | 929 | 10 | 33.8 | 17 | 12 | US-10-342-902-163    | Sequence 163, App |
| C 857 | 10 | 34.5 | 42 | 14 | US-10-298-148-39     | Sequence 39, Appl | 930 | 10 | 33.8 | 17 | 12 | US-10-342-902-1470   | Sequence 1470, Ap |
| C 858 | 10 | 34.5 | 45 | 12 | US-10-278-768-28     | Sequence 28, Appl | 931 | 10 | 33.8 | 17 | 12 | US-10-675-685-281    | Sequence 281, App |
| C 859 | 10 | 34.5 | 45 | 14 | US-10-151-716-11     | Sequence 11, Appl | 932 | 10 | 33.8 | 17 | 12 | US-10-675-685-282    | Sequence 282, App |
| C 860 | 10 | 34.5 | 45 | 9  | US-09-978-274A-22    | Sequence 22, Appl | 933 | 10 | 33.8 | 17 | 12 | US-10-675-685-283    | Sequence 283, App |
| C 861 | 10 | 34.5 | 47 | 14 | US-10-263-103-6      | Sequence 6, Appli | 934 | 10 | 33.8 | 17 | 14 | US-10-339-793-396    | Sequence 396, App |
| C 862 | 10 | 34.5 | 47 | 14 | US-10-263-103-7      | Sequence 7, Appli | 935 | 10 | 33.8 | 18 | 15 | US-10-349-143-5466   | Sequence 5466, Ap |
| C 863 | 10 | 34.5 | 47 | 15 | US-10-349-143-1676   | Sequence 1676, Ap | 936 | 10 | 33.8 | 18 | 15 | US-10-349-143-7686   | Sequence 7686, Ap |
| C 864 | 10 | 34.5 | 47 | 15 | US-10-349-143-2668   | Sequence 2668, Ap | 937 | 10 | 33.8 | 19 | 10 | US-09-911-226-7      | Sequence 7, Appli |
| C 865 | 10 | 34.5 | 47 | 15 | US-10-349-143-2903   | Sequence 2903, Ap | 938 | 10 | 33.8 | 19 | 12 | US-10-700-018-7      | Sequence 7, Appli |
| C 866 | 10 | 34.5 | 49 | 8  | US-09-962-537-46     | Sequence 46, Appl | 939 | 10 | 33.8 | 19 | 15 | US-10-349-143-4780   | Sequence 4780, Ap |
| C 867 | 10 | 34.5 | 50 | 8  | US-08-781-986A-2247  | Sequence 2247, Ap | 940 | 10 | 33.8 | 19 | 15 | US-10-349-143-5884   | Sequence 5884, Ap |
| C 868 | 10 | 34.5 | 50 | 12 | US-10-329-624-2247   | Sequence 2247, Ap | 941 | 10 | 33.8 | 20 | 12 | US-10-376-323-69     | Sequence 69, Appl |
| C 869 | 10 | 34.5 | 50 | 15 | US-10-131-827-6087   | Sequence 6087, Ap | 942 | 10 | 33.8 | 20 | 14 | US-10-012-984-44     | Sequence 44, Appl |
| C 870 | 10 | 34.5 | 50 | 15 | US-10-131-827-7657   | Sequence 7657, Ap | 943 | 10 | 33.8 | 20 | 14 | US-10-008-789-78     | Sequence 78, Appl |
| C 871 | 10 | 34.5 | 52 | 12 | US-10-027-632-176418 | Sequence 176418,  | 944 | 10 | 33.8 | 20 | 14 | US-10-279-964-3      | Sequence 3, Appli |
| C 872 | 10 | 34.5 | 52 | 15 | US-10-027-632-176418 | Sequence 176418,  | 945 | 10 | 33.8 | 20 | 15 | US-10-289-762-3600   | Sequence 3600, Ap |
| C 873 | 10 | 34.5 | 53 | 10 | US-09-918-156-62     | Sequence 62, Appl | 946 | 10 | 33.8 | 20 | 15 | US-10-138-588-159    | Sequence 159, App |
| C 874 | 10 | 34.5 | 60 | 10 | US-09-918-740-30     | Sequence 30, Appl | 947 | 10 | 33.8 | 20 | 16 | US-10-210-429-45     | Sequence 45, Appl |
| C 875 | 10 | 34.5 | 60 | 10 | US-09-908-975-8204   | Sequence 8204, Ap | 948 | 10 | 33.8 | 20 | 16 | US-10-210-429-116    | Sequence 116, App |
| C 876 | 10 | 34.5 | 60 | 10 | US-09-908-975-9728   | Sequence 9728, Ap | 949 | 10 | 33.8 | 21 | 9  | US-09-765-081-363    | Sequence 363, App |
| C 877 | 10 | 34.5 | 60 | 10 | US-09-908-975-9757   | Sequence 9757, Ap | 950 | 10 | 33.8 | 21 | 9  | US-09-815-156-4      | Sequence 4, Appli |
| C 878 | 10 | 34.5 | 60 | 10 | US-09-908-975-13703  | Sequence 13703, A | 951 | 10 | 33.8 | 21 | 10 | US-09-229-751A-2     | Sequence 2, Appli |
| C 879 | 10 | 34.5 | 60 | 10 | US-09-908-975-14132  | Sequence 14132, A | 952 | 10 | 33.8 | 21 | 10 | US-09-988-626-153    | Sequence 153, App |
| C 880 | 10 | 34.5 | 60 | 10 | US-09-908-975-14399  | Sequence 14399, A | 953 | 10 | 33.8 | 21 | 10 | US-09-988-687-153    | Sequence 153, App |
| C 881 | 10 | 34.5 | 60 | 10 | US-09-908-975-14520  | Sequence 14520, A | 954 | 10 | 33.8 | 21 | 10 | US-09-988-686-153    | Sequence 153, App |
| C 882 | 10 | 34.5 | 60 | 10 | US-09-908-975-15007  | Sequence 15007, A | 955 | 10 | 33.8 | 21 | 13 | US-10-075-425-3      | Sequence 3, Appli |
| C 883 | 10 | 34.5 | 60 | 10 | US-09-908-975-15248  | Sequence 15248, A | 956 | 10 | 33.8 | 22 | 9  | US-09-870-745-9      | Sequence 9, Appli |
| C 884 | 10 | 34.5 | 60 | 10 | US-09-908-975-18236  | Sequence 18236, A | 957 | 10 | 33.8 | 22 | 9  | US-09-810-993-6      | Sequence 6, Appli |
| C 885 | 10 | 34.5 | 60 | 10 | US-09-908-975-20732  | Sequence 20732, A | 958 | 10 | 33.8 | 22 | 9  | US-09-810-993-19     | Sequence 19, Appl |
| C 886 | 10 | 34.5 | 60 | 10 | US-09-908-975-20766  | Sequence 20766, A | 959 | 10 | 33.8 | 22 | 14 | US-10-151-484-27     | Sequence 27, Appl |
| C 887 | 10 | 34.5 | 60 | 13 | US-09-908-975-21435  | Sequence 21435, A | 960 | 10 | 33.8 | 22 | 14 | US-10-251-210-6      | Sequence 6, Appli |
| C 888 | 10 | 34.5 | 60 | 14 | US-10-025-367-19     | Sequence 19, Appl | 961 | 10 | 33.8 | 22 | 14 | US-10-251-210-19     | Sequence 19, Appl |
| C 889 | 10 | 34.5 | 60 | 14 | US-10-099-382-6      | Sequence 6, Appli | 962 | 10 | 33.8 | 22 | 14 | US-10-284-249-34     | Sequence 34, Appl |
| C 890 | 10 | 34.5 | 60 | 14 | US-10-099-382-7      | Sequence 7, Appli | 963 | 10 | 33.8 | 23 | 13 | US-10-127-391-22     | Sequence 22, Appl |
| C 891 | 10 | 34.5 | 61 | 14 | US-10-349-508-66     | Sequence 66, Appl | 964 | 10 | 33.8 | 23 | 14 | US-10-241-332-22     | Sequence 22, Appl |

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|-------|-----|------|----|----|----------------------|-------------------|
| C 965 | 9 8 | 33 8 | 24 | 10 | US-09-940-185-3218   | Sequence 3218, Ap |
| C 966 | 9 8 | 33 8 | 24 | 14 | US-10-004-551-97     | Sequence 97, Appl |
| C 967 | 9 8 | 33 8 | 25 | 9  | US-09-866-108-15100  | Sequence 15100, A |
| C 968 | 9 8 | 33 8 | 25 | 9  | US-09-866-108-15101  | Sequence 15101, A |
| C 969 | 9 8 | 33 8 | 25 | 9  | US-09-866-108-15102  | Sequence 15102, A |
| C 970 | 9 8 | 33 8 | 25 | 9  | US-09-866-108-15103  | Sequence 15103, A |
| C 971 | 9 8 | 33 8 | 25 | 9  | US-09-866-108-15104  | Sequence 15104, A |
| C 972 | 9 8 | 33 8 | 25 | 9  | US-09-866-108-15105  | Sequence 15105, A |
| C 973 | 9 8 | 33 8 | 25 | 9  | US-09-866-108-15106  | Sequence 15106, A |
| C 974 | 9 8 | 33 8 | 25 | 9  | US-09-866-108-15107  | Sequence 15107, A |
| C 975 | 9 8 | 33 8 | 25 | 9  | US-09-866-108-15108  | Sequence 15108, A |
| C 976 | 9 8 | 33 8 | 25 | 9  | US-09-866-108-15109  | Sequence 15109, A |
| C 977 | 9 8 | 33 8 | 25 | 9  | US-09-837-998-1096   | Sequence 1096, Ap |
| C 978 | 9 8 | 33 8 | 25 | 9  | US-09-837-998-1105   | Sequence 1105, Ap |
| C 979 | 9 8 | 33 8 | 25 | 9  | US-09-837-998-1106   | Sequence 1106, Ap |
| C 980 | 9 8 | 33 8 | 25 | 12 | US-10-675-685-1096   | Sequence 1096, Ap |
| C 981 | 9 8 | 33 8 | 25 | 12 | US-10-675-685-1105   | Sequence 1105, Ap |
| C 982 | 9 8 | 33 8 | 25 | 12 | US-10-675-685-1106   | Sequence 1106, Ap |
| C 983 | 9 8 | 33 8 | 25 | 14 | US-10-143-849-18     | Sequence 18, Appl |
| C 984 | 9 8 | 33 8 | 25 | 14 | US-10-215-112-6496   | Sequence 6496, Ap |
| C 985 | 9 8 | 33 8 | 25 | 14 | US-10-215-112-6522   | Sequence 6522, Ap |
| C 986 | 9 8 | 33 8 | 25 | 14 | US-10-098-263B-3507  | Sequence 2507, Ap |
| C 987 | 9 8 | 33 8 | 25 | 14 | US-10-098-263B-5480  | Sequence 5480, Ap |
| C 988 | 9 8 | 33 8 | 25 | 14 | US-10-098-263B-6121  | Sequence 6121, Ap |
| C 989 | 9 8 | 33 8 | 25 | 14 | US-10-098-263B-8809  | Sequence 8809, Ap |
| C 990 | 9 8 | 33 8 | 25 | 14 | US-10-098-263B-8995  | Sequence 8995, Ap |
| C 991 | 9 8 | 33 8 | 25 | 14 | US-10-098-263B-20144 | Sequence 20144, A |
| C 992 | 9 8 | 33 8 | 25 | 14 | US-10-098-263B-23117 | Sequence 23117, A |
| C 993 | 9 8 | 33 8 | 25 | 14 | US-10-098-263B-30083 | Sequence 30083, A |
| C 994 | 9 8 | 33 8 | 25 | 14 | US-10-098-263B-30084 | Sequence 30084, A |
| C 995 | 9 8 | 33 8 | 25 | 14 | US-10-098-263B-35561 | Sequence 35561, A |
| C 996 | 9 8 | 33 8 | 25 | 14 | US-10-098-263B-36050 | Sequence 36050, A |
| C 997 | 9 8 | 33 8 | 25 | 14 | US-10-098-263B-43771 | Sequence 43771, A |
| C 998 | 9 8 | 33 8 | 25 | 14 | US-10-098-263B-43887 | Sequence 43887, A |
| C 999 | 9 8 | 33 8 | 25 | 14 | US-10-098-263B-43888 | Sequence 43888, A |
| 1000  | 9 8 | 33 8 | 25 | 14 | US-10-098-263B-43912 | Sequence 43912, A |

## ALIGNMENTS

RESULT 1  
 US-10-335-977-10024  
 Sequence 10024, Application US/10335977  
 Publication No. US20040052799A1  
 GENERAL INFORMATION:  
 APPLICANT: DOUGLAS SMITH et al  
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES  
 RELATING TO HELICOBACTER PYLORI FOR  
 DIAGNOSTICS AND THERAPEUTICS  
 NUMBER OF SEQUENCES: 10031  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: LAHIVE & COCKFIELD  
 STREET: 28 State Street  
 CITY: Boston  
 STATE: Massachusetts  
 COUNTRY: USA  
 ZIP: 02109-1875  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: CD/ROM ISO9660  
 COMPUTER: IBM PC Compatible  
 OPERATING SYSTEM: Windows NT 4.0  
 SOFTWARE: UNIX  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/10/335,977  
 FILING DATE: 30-Dec-2002  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/993,002  
 FILING DATE: 17-Dec-1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Mandragouras, Amy E.  
 REGISTRATION NUMBER: 36,207  
 REFERENCE/DOCKET NUMBER: GTN-018

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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 10024:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM SOURCE: Helicobacter pylori
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...30
; SEQUENCE DESCRIPTION: SEQ ID NO: 10024:
US-10-335-977-10024

Query Match 44.1%; Score 12.8; D
Best Local Similarity 50.0%; Pred. No. 2.3e
Matches 10; Conservative 4; Mismatches

QY 4 GAUNCUUNNGUAGCCCA 23
|||:|:|:|:|:|:|:|
DB 5 GATCCTTAGCAGCTCAA 24

RESULT 2
US-08-781-986A-2762
; Sequence 2762, Application US/08781986A
; Publication No. US20030054436A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 2762:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 68 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-781-986A-2762

Query Match 44.1%; Score 12.8; D
Best Local Similarity 47.6%; Pred. No. 2.6e

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Matches 10; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 5 AUNCUUNNGUAGCCCNANG 25  
| : : : : :  
Db 3 ATCCTGTTCTAGCCGACG 23

RESULT 3  
US-10-329-624-2762  
; Sequence 2762, Application US/10329624  
; Publication No. US20040043037A1  
; GENERAL INFORMATION:  
; APPLICANT: Charles Kunsch  
; Gil H. Choi  
; Patrick S. Dillon  
; Craig A. Rosen  
; Steven C. Barash  
; Michael R. Fannon  
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences  
; NUMBER OF SEQUENCES: 5256  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: Maryland  
; COUNTRY: USA  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage  
; COMPUTER: HP Vectra 486/33  
; OPERATING SYSTEM: MSDOS version 6.2  
; SOFTWARE: ASCII Text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/329,624  
; FILING DATE: 27-Dec-2002  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/956,171  
; FILING DATE: October 20, 1997  
; APPLICATION NUMBER: 60/009,861  
; FILING DATE: January 5, 1996  
; APPLICATION NUMBER: 08/781,986  
; FILING DATE: January 3, 1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mark J. Hyman  
; REGISTRATION NUMBER: 46,789  
; REFERENCE/DOCKET NUMBER: PB248P1D1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (240) 314-1224  
; TELEFAX: (301) 309-8439  
; INFORMATION FOR SEQ ID NO: 2762:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 68 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 2762:  
US-10-329-624-2762

Query Match 44.1%; Score 12.8; DB 12; Length 68;  
Best Local Similarity 47.6%; Pred. No. 2.6e+03;  
Matches 10; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 5 AUNCUUNNGUAGCCCNANG 25  
| : : : : :  
Db 3 ATCCTGTTCTAGCCGACG 23

RESULT 4  
US-09-908-975-18725/c  
; Sequence 18725, Application US/09908975  
; Publication No. US20030165843A1  
; GENERAL INFORMATION:  
; APPLICANT: SHOSHAN, Avi

Matches 10; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

; APPLICANT: WASSERMAN, Alon  
; APPLICANT: MINTZ, Eli  
; APPLICANT: MINTZ, Liat  
; APPLICANT: FAIGLER, Simchon  
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE  
; FILE OF INVENTION: THAT POPULATE A TRANSCRIPTOME  
; FILE REFERENCE: 36688-0005  
; CURRENT APPLICATION NUMBER: US/09/908,975  
; CURRENT FILING DATE: 2001-07-20  
; PRIOR APPLICATION NUMBER: US 60/287,724  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: US 60/221,607  
; PRIOR FILING DATE: 2000-07-28  
; NUMBER OF SEQ ID NOS: 32337  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 18725  
; LENGTH: 60  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-908-975-18725

Query Match 42.8%; Score 12.4; DB 10; Length 60;  
Best Local Similarity 55.6%; Pred. No. 4.4e+03;  
Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 8 CUUUNNGUAGCCCNANG 25  
| : : : : :  
Db 25 CTTTCTGAAGCCCATG 8

RESULT 5  
US-09-908-975-2848/c  
; Sequence 2848, Application US/09908975  
; Publication No. US20030165843A1  
; GENERAL INFORMATION:  
; APPLICANT: SHOSHAN, Avi  
; APPLICANT: WASSERMAN, Alon  
; APPLICANT: MINTZ, Eli  
; APPLICANT: MINTZ, Liat  
; APPLICANT: FAIGLER, Simchon  
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE  
; FILE OF INVENTION: THAT POPULATE A TRANSCRIPTOME  
; FILE REFERENCE: 36688-0005  
; CURRENT APPLICATION NUMBER: US/09/908,975  
; CURRENT FILING DATE: 2001-07-20  
; PRIOR APPLICATION NUMBER: US 60/287,724  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: US 60/221,607  
; PRIOR FILING DATE: 2000-07-28  
; NUMBER OF SEQ ID NOS: 32337  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2848  
; LENGTH: 65  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
US-09-908-975-2848

Query Match 42.8%; Score 12.4; DB 10; Length 65;  
Best Local Similarity 52.9%; Pred. No. 4.4e+03;  
Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 4 GAUNCUUNNGUAGCC 20  
| : : : : :  
Db 53 GATACTTCAGTAAGCC 37

RESULT 6  
US-10-131-827-464  
; Sequence 464, Application US/10131827  
; Publication No. US20040009479A1  
; GENERAL INFORMATION:  
; APPLICANT: Wohlgenuth, Jay  
; APPLICANT: Fry, Kirk

```
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131.827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 464
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-464

Query Match      42.1%; Score 12.2; DB 15; Length 50;
Best Local Similarity 45.5%; Pred. No. 5.5e+03;
Matches 10; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY      4 GAUNCUUNNGUAGCCCNANG 25
      |||::: ||| |||
Db      22 GAGGCTTTCTAAGCCCAAGG 43

RESULT 7
US-09-908-975-9828
; Sequence 9828, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Liat
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9828
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975-9828

Query Match      42.1%; Score 12.2; DB 10; Length 60;
Best Local Similarity 52.2%; Pred. No. 5.7e+03;
Matches 12; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

QY      5 AUNCUUNNGUAGCCCNANG 27
      |||::: ||| |||
Db      34 AACCTCATGTAAGCCCAAGG 56

RESULT 8
US-09-908-975-12187/c
; Sequence 12187, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Liat
```

```
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
; TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12187
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975-12187

Query Match      42.1%; Score 12.2; DB 10; Length 60;
Best Local Similarity 40.9%; Pred. No. 5.7e+03;
Matches 9; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY      4 GAUNCUUNNGUAGCCCNANG 25
      |||::: ||| |||
Db      54 GATTCTTCTAGCGCTAAG 33

RESULT 9
US-09-908-975-15109/c
; Sequence 15109, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Liat
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15109
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975-15109

Query Match      42.1%; Score 12.2; DB 10; Length 60;
Best Local Similarity 45.5%; Pred. No. 5.7e+03;
Matches 10; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY      4 GAUNCUUNNGUAGCCCNANG 25
      |||::: ||| |||
Db      37 GATGCTTCTGATGGCCAAGG 16

RESULT 10
US-09-908-975-18934
; Sequence 18934, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Liat
; APPLICANT: FAIGLER, Simchon
```

```
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
; TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 18934
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975-18934

Query Match      42.1%; Score 12.2; DB 10; Length 60;
Best Local Similarity 43.5%; Pred. No. 5.7e+03;
Matches 10; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY      5 AUNCUUNNGUAGCCCNANGNG 27
      ||:|:|:|:|:|:|:|:|:|
DB      27 ATCCGTTGCGTARGACAGAG 49

RESULT 11
US-10-098-263B-76444
; Sequence 76444, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 76444
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-76444

Query Match      40.7%; Score 11.8; DB 14; Length 25;
Best Local Similarity 44.4%; Pred. No. 8.4e+03;
Matches 8; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY      4 GAUNCUUNNGUAGCCCC 21
      ||:|:|:|:|:|:|
DB      1 GATACCTTTTAAAGTCC 18

RESULT 12
US-09-230-926A-35
; Sequence 35, Application US/09230926A
; Patent No. US20020168633A1
; GENERAL INFORMATION:
; APPLICANT: WABILIAT, Claude
; APPLICANT: SCHLEIFER, Karl-Heinz
; APPLICANT: LUDWIG, Wolfgang
; TITLE OF INVENTION: NUCLEOTIDE FRAGMENT OF THE 23S RNA OF BACTERIA OF THE GENUS CHLAMYDIA
; TITLE OF INVENTION: USE AS A PROBE, PRIMER, AND IN A REAGENT AND A DETECTION PROCEDURE
; FILE REFERENCE: 102682
; CURRENT APPLICATION NUMBER: US/09/230,926A
; CURRENT FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: PCT/FR98/01157
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: FR 97/07200
; PRIOR FILING DATE: 1997-06-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.0
```

```
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
; LENGTH: 47
; TYPE: RNA
; ORGANISM: Chlamydia pneumoniae
US-09-230-926A-35

Query Match      40.7%; Score 11.8; DB 9; Length 47;
Best Local Similarity 65.0%; Pred. No. 9.3e+03;
Matches 13; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY      6 UNCUCUUNNGUAGCCCNANG 25
      ||:|:|:|:|:|:|
DB      28 UCCUCGCGUAGCCCAAGG 47

RESULT 13
US-09-908-975-15914/c
; Sequence 15914, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Liat
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15914
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975-15914

Query Match      40.7%; Score 11.8; DB 10; Length 60;
Best Local Similarity 50.0%; Pred. No. 9.7e+03;
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY      4 GAUNCUUNNGUAGCCCC 21
      ||:|:|:|:|:|:|
DB      30 GAGCGTTTGAGTGAGCCC 13

RESULT 14
US-09-908-975-17626
; Sequence 17626, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Liat
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
```

SEQ ID NO 17626  
LENGTH: 60  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-908-975-17626

Query Match 40.7%; Score 11.8; DB 10; Length 60;  
Best Local Similarity 40.0%; Pred. No. 9.7e+03;  
Matches 8; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 6 UCUUUNGUAGCCCNANG 25  
: : : : :  
Db 28 TGTCTTTGGTAAGCACTTGG 47

RESULT 15  
US-09-908-975-1254  
Sequence 1254, Application US/09908975  
Publication No. US20030165843A1  
GENERAL INFORMATION:  
APPLICANT: SHOSHAN, Avi  
APPLICANT: WASSERMAN, Alon  
APPLICANT: MINTZ, Eli  
APPLICANT: FAIGLER, Simchon  
TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE  
FILE REFERENCE: 36688-0005  
CURRENT APPLICATION NUMBER: US/09/908,975  
CURRENT FILING DATE: 2001-07-20  
PRIOR APPLICATION NUMBER: US 60/287,724  
PRIOR FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: US 60/221,607  
PRIOR FILING DATE: 2000-07-28  
NUMBER OF SEQ ID NOS: 32337  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 1254  
LENGTH: 65  
TYPE: DNA  
ORGANISM: Rattus norvegicus  
US-09-908-975-1254

Query Match 40.7%; Score 11.8; DB 10; Length 65;  
Best Local Similarity 45.0%; Pred. No. 9.8e+03;  
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 6 UCUUUNGUAGCCCNANG 25  
: : : : :  
Db 11 TGTCTTTGGTAAGTCCAGG 30

RESULT 16  
US-09-908-975-30297  
Sequence 30297, Application US/09908975  
Publication No. US20030165843A1  
GENERAL INFORMATION:  
APPLICANT: SHOSHAN, Avi  
APPLICANT: WASSERMAN, Alon  
APPLICANT: MINTZ, Eli  
APPLICANT: FAIGLER, Simchon  
TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE  
FILE REFERENCE: 36688-0005  
CURRENT APPLICATION NUMBER: US/09/908,975  
CURRENT FILING DATE: 2001-07-20  
PRIOR APPLICATION NUMBER: US 60/287,724  
PRIOR FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: US 60/221,607  
PRIOR FILING DATE: 2000-07-28  
NUMBER OF SEQ ID NOS: 32337  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 30297

LENGTH: 65  
TYPE: DNA  
ORGANISM: Mus musculus  
US-09-908-975-30297

Query Match 40.7%; Score 11.8; DB 10; Length 65;  
Best Local Similarity 50.0%; Pred. No. 9.8e+03;  
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 4 GAUNCUUNNGUAGGCC 21  
: : : : :  
Db 37 GATTCITTTCCCAAGCCC 54

RESULT 17  
US-10-032-585-316  
Sequence 316, Application US/10032585  
Publication No. US20030180953A1  
GENERAL INFORMATION:  
APPLICANT: Terry, Roemer D.  
APPLICANT: Bo, Jiang  
APPLICANT: Charles, Boone  
APPLICANT: Howard, Bussey  
TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery  
FILE REFERENCE: 10182-006-999  
CURRENT APPLICATION NUMBER: US/10/032,585  
CURRENT FILING DATE: 2001-12-20  
NUMBER OF SEQ ID NOS: 8000  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 316  
LENGTH: 65  
TYPE: DNA  
ORGANISM: Candida albicans  
US-10-032-585-316

Query Match 40.7%; Score 11.8; DB 14; Length 65;  
Best Local Similarity 42.1%; Pred. No. 9.8e+03;  
Matches 8; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 5 AUNCUUNNGUAGCCCA 23  
: : : : :  
Db 14 ATACTTCAGTATACCAA 32

RESULT 18  
US-09-738-968-9/c  
Sequence 9, Application US/09738968  
Patent No. US20010037016A1  
GENERAL INFORMATION:  
APPLICANT: Contag, Pamela R.  
APPLICANT: Purchio, Anthony  
APPLICANT: Zhang, Ning  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SCREENING FOR ANGIOGENESIS  
FILE REFERENCE: 9400-0012.20  
CURRENT APPLICATION NUMBER: US/09/738,968  
CURRENT FILING DATE: 2001-05-11  
PRIOR APPLICATION NUMBER: 09/465,978  
PRIOR FILING DATE: 1999-12-16  
NUMBER OF SEQ ID NOS: 45  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 9  
LENGTH: 77  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: primer F3R31  
US-09-738-968-9

Query Match 40.7%; Score 11.8; DB 9; Length 77;  
Best Local Similarity 50.0%; Pred. No. 1e+04; 5; Indels 0; Gaps 0;  
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 4 GAUNCUUNNGUAGAGCC 21  
||: ||: : |||||  
Db 23 GATGCAATTAATTAAGCC 6

## RESULT 19

US-09-738-968-10  
; Sequence 10, Application US/09738968  
; Patent No. US20010037016A1  
; GENERAL INFORMATION:  
; APPLICANT: Contag, Pamela R.  
; APPLICANT: Purchio, Anthony  
; APPLICANT: Zhang, Ning  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SCREENING FOR ANGIOGENESIS  
; TITLE OF INVENTION: MODULATING COMPOUNDS  
; FILE REFERENCE: 9400-0012.20  
; CURRENT APPLICATION NUMBER: US/09/738,968  
; CURRENT FILING DATE: 2001-05-11  
; PRIOR APPLICATION NUMBER: 09/465,978  
; PRIOR FILING DATE: 1999-12-16  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 10  
; LENGTH: 77  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: primer P3R32  
US-09-738-968-10

Query Match 40.7%; Score 11.8; DB 9; Length 77;  
Best Local Similarity 50.0%; Pred. No. 1e+04;  
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 4 GAUNCUUNNGUAGAGCC 21  
||: ||: : |||||  
Db 59 GATGCAATTAATTAAGCC 76

## RESULT 20

US-09-964-895-27  
; Sequence 27, Application US/09964895  
; Publication No. US20030099667A1  
; GENERAL INFORMATION:  
; APPLICANT: Zeon Corporation  
; TITLE OF INVENTION: Avian herpesvirus-based recombinant Gumboro disease  
; TITLE OF INVENTION: vaccine  
; FILE REFERENCE: zHVT/IBD-E  
; CURRENT APPLICATION NUMBER: US/09/964,895  
; CURRENT FILING DATE: 2001-09-28  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 27  
; LENGTH: 24  
; TYPE: DNA  
; ORGANISM: Gallid herpesvirus 2  
US-09-964-895-27

Query Match 40.0%; Score 11.6; DB 10; Length 24;  
Best Local Similarity 45.8%; Pred. No. 1.1e+04;  
Matches 11; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 4 GAUNCUUNNGUAGAGCCNANG 27  
||: ||: : |||||  
Db 1 GGTGCAATTCGTAAGACCGATGG 24

## RESULT 21

US-10-059-152-26  
; Sequence 26, Application US/10059152  
; Publication No. US20030157703A1  
; GENERAL INFORMATION:  
; APPLICANT: Zeon Corporation

; TITLE OF INVENTION: Recombinant herpesvirus of turkeys and use thereof  
; FILE REFERENCE: NDV  
; CURRENT APPLICATION NUMBER: US/10/059,152  
; CURRENT FILING DATE: 2001-01-31  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 26  
; LENGTH: 24  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: primer DNA for PCR  
US-10-059-152-26

Query Match 40.0%; Score 11.6; DB 14; Length 24;  
Best Local Similarity 45.8%; Pred. No. 1.1e+04;  
Matches 11; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 4 GAUNCUUNNGUAGCCNANG 27  
||: ||: : |||||  
Db 1 GGTGCAATTCGTAAGACCGATGG 24

## RESULT 22

US-09-848-754A-6937/c  
; Sequence 6937, Application US/09848754A  
; Publication No. US20030073207A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relat  
; TITLE OF INVENTION: Levels of Epidermal Growth Factor Receptors  
; FILE REFERENCE: MBH00-958-1 (400/018)  
; CURRENT APPLICATION NUMBER: US/09/848,754A  
; CURRENT FILING DATE: 2001-05-03  
; NUMBER OF SEQ ID NOS: 9645  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 6937  
; LENGTH: 31  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic acid  
US-09-848-754A-6937

Query Match 40.0%; Score 11.6; DB 10; Length 31;  
Best Local Similarity 45.8%; Pred. No. 1.1e+04;  
Matches 11; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 4 GAUNCUUNNGUAGCCNANG 27  
||: ||: : |||||  
Db 25 GATCGTTAGCTAGCCCCAAGG 2

## RESULT 23

US-09-848-754A-7188/c  
; Sequence 7188, Application US/09848754A  
; Publication No. US20030073207A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relat  
; TITLE OF INVENTION: Levels of Epidermal Growth Factor Receptors  
; FILE REFERENCE: MBH00-958-1 (400/018)  
; CURRENT APPLICATION NUMBER: US/09/848,754A  
; CURRENT FILING DATE: 2001-05-03  
; NUMBER OF SEQ ID NOS: 9645  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 7188  
; LENGTH: 31  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic acid  
US-09-848-754A-7188



US-09-848-754A-7188

Query Match 40.0%; Score 11.6; DB 10; Length 31;  
Best Local Similarity 45.8%; Pred. No. 1.1e+04;  
Matches 11; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 4 GAUNCUUUNNGUAGGCCCNANGNG 27  
||: : : ||||| |||||  
Db 25 GATCGTTGTAGCTAGCCCTACGGG 2

RESULT 24

US-09-848-754A-7495/c  
; Sequence 7495, Application US/09848754A  
; Publication No. US20030073207A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related  
; FILE REFERENCE: MBH00-958-I (400/018)  
; CURRENT APPLICATION NUMBER: US/09/848,754A  
; CURRENT FILING DATE: 2001-05-03  
; NUMBER OF SEQ ID NOS: 9645  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 7495  
; LENGTH: 31  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic acid  
US-09-848-754A-7495

Query Match 40.0%; Score 11.6; DB 10; Length 31;  
Best Local Similarity 45.8%; Pred. No. 1.1e+04;  
Matches 11; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 4 GAUNCUUUNNGUAGGCCCNANGNG 27  
||: : : ||||| |||||  
Db 25 GATCGTTGTAGCTAGCCCAAGGAG 2

RESULT 25

US-09-740-332-6639/c  
; Sequence 6639, Application US/09740332  
; Publication No. US20030125270A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals Inc.  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related  
; FILE REFERENCE: RPI 400/003  
; CURRENT APPLICATION NUMBER: US/09/740,332  
; CURRENT FILING DATE: 2001-03-26  
; NUMBER OF SEQ ID NOS: 9704  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 6639  
; LENGTH: 31  
; TYPE: DNA  
; ORGANISM: artificial sequence  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION:  
; OTHER INFORMATION: DNazyme  
US-09-740-332-6639

Query Match 40.0%; Score 11.6; DB 10; Length 31;  
Best Local Similarity 45.8%; Pred. No. 1.1e+04;  
Matches 11; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 4 GAUNCUUUNNGUAGGCCCNANGNG 27  
||: : : ||||| |||||  
Db 25 GATCGTTGTAGCTAGCCCAAGGAG 2

RESULT 26

US-09-740-332-9154/c  
; Sequence 9154, Application US/09740332  
; Publication No. US20030125270A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals Inc.  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related  
; FILE REFERENCE: RPI 400/003  
; CURRENT APPLICATION NUMBER: US/09/740,332  
; CURRENT FILING DATE: 2001-03-26  
; NUMBER OF SEQ ID NOS: 9704  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 9154  
; LENGTH: 31  
; TYPE: DNA  
; ORGANISM: artificial sequence  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION:  
; OTHER INFORMATION: DNazyme  
US-09-740-332-9154

Query Match 40.0%; Score 11.6; DB 10; Length 31;  
Best Local Similarity 45.8%; Pred. No. 1.1e+04;  
Matches 11; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 4 GAUNCUUUNNGUAGGCCCNANGNG 27  
||: : : ||||| |||||  
Db 25 GATCGTTGTAGCTAGCCCAAGGAG 2

RESULT 27

US-09-817-879-6639/c  
; Sequence 6639, Application US/09817879  
; Publication No. US20030171311A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals Inc.  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related  
; FILE REFERENCE: MBH00-801-F  
; CURRENT APPLICATION NUMBER: US/09/817,879  
; CURRENT FILING DATE: 2001-03-26  
; NUMBER OF SEQ ID NOS: 9703  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 6639  
; LENGTH: 31  
; TYPE: DNA  
; ORGANISM: artificial sequence  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION:  
; OTHER INFORMATION: DNazyme  
US-09-817-879-6639

Query Match 40.0%; Score 11.6; DB 10; Length 31;  
Best Local Similarity 45.8%; Pred. No. 1.1e+04;  
Matches 11; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 4 GAUNCUUUNNGUAGGCCCNANGNG 27  
||: : : ||||| |||||  
Db 25 GATCGTTGTAGCTAGCCCAAGGAG 2

RESULT 28

US-09-817-879-9154/c  
; Sequence 9154, Application US/09817879  
; Publication No. US20030171311A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals Inc.  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related  
; FILE REFERENCE: MBH00-801-F



Db 8 GTTGCTCTGGTAAAGCTCGACGAG 31

## RESULT 33

US-09-800-130A-8/c  
; Sequence 8, Application US/09800130A  
; Publication No. US20030188346A1  
; GENERAL INFORMATION:  
; APPLICANT: Baerson, Scott  
; APPLICANT: Heck, Gregory  
; APPLICANT: Rodriguez, Damian  
; TITLE OF INVENTION: Methods for Making Plants Tolerant to Glyphosate and Compositions  
; FILE REFERENCE: 60/188,093  
; CURRENT APPLICATION NUMBER: US/09/800,130A  
; CURRENT FILING DATE: 2001-03-06  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 8  
; LENGTH: 56  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; NAME/KEY: 5'UTR  
; LOCATION: (1)..(56)  
; OTHER INFORMATION: fully synthetic DNA leader sequence  
US-09-800-130A-8

Query Match 40.0%; Score 11.6; DB 10; Length 56;

Best Local Similarity 41.7%; Pred. No. 1.3e+04;  
Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 4 GAUNCUUUNNGUAGCCCNANGNG 27

Db 28 GCTTAATTAATTAAGCCCTAGGAG 5

## RESULT 34

US-10-413-909-8/c  
; Sequence 8, Application US/10413909  
; Publication No. US20030192072A1  
; GENERAL INFORMATION:  
; APPLICANT: Baerson, Scott  
; APPLICANT: Heck, Gregory  
; APPLICANT: Rodriguez, Damian  
; TITLE OF INVENTION: Methods for Making Plants Tolerant to Glyphosate and Compositions  
; FILE REFERENCE: 11898.0019.00DVUS01 (MOBS019--1)  
; CURRENT APPLICATION NUMBER: US/10/413,909  
; CURRENT FILING DATE: 2003-04-15  
; PRIOR APPLICATION NUMBER: 60/188,093  
; PRIOR FILING DATE: 2000-03-09  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 8  
; LENGTH: 56  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: fully synthetic DNA leader sequence  
; NAME/KEY: 5'UTR  
; LOCATION: (1)..(56)  
; OTHER INFORMATION: fully synthetic DNA leader sequence  
US-10-413-909-8

Query Match 40.0%; Score 11.6; DB 14; Length 56;

Best Local Similarity 41.7%; Pred. No. 1.3e+04;  
Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 4 GAUNCUUUNNGUAGCCCNANGNG 27

Db 28 GCTTAATTAATTAAGCCCTAGGAG 5

## RESULT 35

US-09-908-975-5781  
; Sequence 5781, Application US/09908975  
; Publication No. US20030165843A1  
; GENERAL INFORMATION:  
; APPLICANT: SHOSHAN, Avi  
; APPLICANT: WASSERMAN, Alon  
; APPLICANT: MINTZ, Eli  
; APPLICANT: MINTZ, Liat  
; APPLICANT: FAIGLER, Simchon  
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE  
; FILE REFERENCE: 36688-0005  
; CURRENT APPLICATION NUMBER: US/09/908,975  
; CURRENT FILING DATE: 2001-07-20  
; PRIOR APPLICATION NUMBER: US 60/287,724  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: US 60/221,607  
; PRIOR FILING DATE: 2000-07-28  
; NUMBER OF SEQ ID NOS: 32337  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 5781  
; LENGTH: 60  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-908-975-5781

Query Match 40.0%; Score 11.6; DB 10; Length 60;

Best Local Similarity 50.0%; Pred. No. 1.3e+04;  
Matches 12; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

QY 4 GAUNCUUUNNGUAGCCCNANGNG 27

Db 7 GAGCTTGTCAGCGAAGCCCTATGTG 30

## RESULT 36

US-09-908-975-12753/c  
; Sequence 12753, Application US/09908975  
; Publication No. US20030165843A1  
; GENERAL INFORMATION:  
; APPLICANT: SHOSHAN, Avi  
; APPLICANT: WASSERMAN, Alon  
; APPLICANT: MINTZ, Eli  
; APPLICANT: MINTZ, Liat  
; APPLICANT: FAIGLER, Simchon  
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE  
; FILE REFERENCE: 36688-0005  
; CURRENT APPLICATION NUMBER: US/09/908,975  
; CURRENT FILING DATE: 2001-07-20  
; PRIOR APPLICATION NUMBER: US 60/287,724  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: US 60/221,607  
; PRIOR FILING DATE: 2000-07-28  
; NUMBER OF SEQ ID NOS: 32337  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 12753  
; LENGTH: 60  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-908-975-12753

Query Match 40.0%; Score 11.6; DB 10; Length 60;

Best Local Similarity 41.7%; Pred. No. 1.3e+04;  
Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 4 GAUNCUUUNNGUAGCCCNANGNG 27

Db 46 GGTTCCTCTGGGTAGCGCAATGTG 23

## RESULT 37

US-09-908-975-14781/c  
; Sequence 14781, Application US/09908975  
; Publication No. US20030165843A1  
; GENERAL INFORMATION:  
; APPLICANT: SHOSHAN, Avi  
; APPLICANT: WASSERMAN, Alon  
; APPLICANT: MINTZ, Eli  
; APPLICANT: MINTZ, Liat  
; APPLICANT: FAIGLER, Simchon  
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE  
; FILE REFERENCE: 36688-0005  
; CURRENT APPLICATION NUMBER: US/09/908,975  
; CURRENT FILING DATE: 2001-07-20  
; PRIOR APPLICATION NUMBER: US 60/287,724  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: US 60/221,607  
; PRIOR FILING DATE: 2000-07-28  
; NUMBER OF SEQ ID NOS: 32337  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 14781  
; LENGTH: 60  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-908-975-14781

Query Match 40.0%; Score 11.6; DB 10; Length 60;  
Best Local Similarity 41.7%; Pred. No. 1.3e+04;  
Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 4 GAUNCUUNNGUAAGCCCNANGNG 27  
|||:::|||||  
DB 45 GACTCTTTGGTTAAGCCTCCTGAG 22

## RESULT 38

US-09-908-975-24835  
; Sequence 24835, Application US/09908975  
; Publication No. US20030165843A1  
; GENERAL INFORMATION:  
; APPLICANT: SHOSHAN, Avi  
; APPLICANT: WASSERMAN, Alon  
; APPLICANT: MINTZ, Eli  
; APPLICANT: MINTZ, Liat  
; APPLICANT: FAIGLER, Simchon  
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE  
; FILE REFERENCE: 36688-0005  
; CURRENT APPLICATION NUMBER: US/09/908,975  
; CURRENT FILING DATE: 2001-07-20  
; PRIOR APPLICATION NUMBER: US 60/287,724  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: US 60/221,607  
; PRIOR FILING DATE: 2000-07-28  
; NUMBER OF SEQ ID NOS: 32337  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 24835  
; LENGTH: 65  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-09-908-975-24835

Query Match 40.0%; Score 11.6; DB 10; Length 65;  
Best Local Similarity 41.7%; Pred. No. 1.3e+04;  
Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 4 GAUNCUUNNGUAAGCCCNANGNG 27  
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DB 5 GATGGGTTCAATATGCCCGAG 28

## RESULT 39

US-09-908-975-29918  
; Sequence 29918, Application US/09908975  
; Publication No. US20030165843A1  
; GENERAL INFORMATION:  
; APPLICANT: SHOSHAN, Avi  
; APPLICANT: WASSERMAN, Alon  
; APPLICANT: MINTZ, Eli  
; APPLICANT: MINTZ, Liat  
; APPLICANT: FAIGLER, Simchon  
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE  
; FILE REFERENCE: 36688-0005  
; CURRENT APPLICATION NUMBER: US/09/908,975  
; CURRENT FILING DATE: 2001-07-20  
; PRIOR APPLICATION NUMBER: US 60/287,724  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: US 60/221,607  
; PRIOR FILING DATE: 2000-07-28  
; NUMBER OF SEQ ID NOS: 32337  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 29918  
; LENGTH: 65  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-09-908-975-29918

Query Match 40.0%; Score 11.6; DB 10; Length 65;  
Best Local Similarity 50.0%; Pred. No. 1.3e+04;  
Matches 12; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

QY 4 GAUNCUUNNGUAAGCCCNANGNG 27  
|||:::|||||  
DB 30 GATCCTGAAGCAAGCCCAAGAAG 53

## RESULT 40

US-10-435-696-279  
; Sequence 279, Application US/10435696  
; Publication No. US20040018525A1  
; GENERAL INFORMATION:  
; APPLICANT: Wirtz, Ralph  
; APPLICANT: Munnes, Marc  
; APPLICANT: Kallabis, Harald  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE PREDICTION, DIAGNOSIS, PROGNOSI  
; FILE REFERENCE: Lea 36 108  
; CURRENT APPLICATION NUMBER: US/10/435,696  
; CURRENT FILING DATE: 2003-05-09  
; PRIOR APPLICATION NUMBER: EP03003112.4  
; PRIOR FILING DATE: 2003-02-13  
; PRIOR APPLICATION NUMBER: EP02010291.9  
; PRIOR FILING DATE: 2002-05-21  
; NUMBER OF SEQ ID NOS: 314  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 279  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: DL7S1955 forward primer  
US-10-435-696-279

Query Match 39.3%; Score 11.4; DB 15; Length 21;  
Best Local Similarity 55.6%; Pred. No. 1.4e+04;  
Matches 10; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 10 UUNNGUAAGCCCNANGNG 27  
:|||||  
DB 3 TAATGTAAGCCCATGAG 20

Search completed: April 18, 2004, 11:55:16  
Job time : 172.667 secs

us-09-310-844c-23.max.rnpb

Tue Apr 20 10:03:02 2004

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OM nucleic - nucleic search, using sw model

Run on: April 18, 2004, 07:34:53 ; Search time 36.6667 Seconds  
(without alignments)  
438.916 Million cell updates/sec

Title: US-09-310-844C-23

Perfect score: 29  
Sequence: 1 nngauncuunngaagccnangnrr. 29

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 915622

Minimum DB seq length: 0  
Maximum DB seq length: 80

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : Issued Patents NA.\*  
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2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq.\*  
3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq.\*  
4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq.\*  
5: /cgn2\_6/ptodata/2/ina/PTUS\_COMB.seq.\*  
6: /cgn2\_6/ptodata/2/ina/backfiles.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description         |
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| 1          | 12.8  | 44.1        | 68     | 4  | US-08-956-171E-2762 |
| 2          | 12.2  | 42.1        | 27     | 6  | Sequence 2762, Ap   |
| 3          | 12.2  | 42.1        | 69     | 2  | Patent No. 5258283  |
| 4          | 12.2  | 42.1        | 69     | 2  | Sequence 30, Appl   |
| 5          | 12.2  | 42.1        | 69     | 2  | Sequence 30, Appl   |
| 6          | 12.2  | 42.1        | 69     | 2  | Sequence 13, Appl   |
| 7          | 11.8  | 40.7        | 21     | 2  | Sequence 10, Appl   |
| 8          | 11.6  | 40.0        | 36     | 4  | Sequence 7, Appl    |
| 9          | 11.6  | 40.0        | 36     | 4  | Sequence 15, Appl   |
| 10         | 11.6  | 40.0        | 36     | 4  | Sequence 7, Appl    |
| 11         | 11.6  | 40.0        | 36     | 5  | Sequence 7, Appl    |
| 12         | 11.6  | 40.0        | 36     | 5  | Sequence 15, Appl   |
| 13         | 11.6  | 40.0        | 61     | 4  | Sequence 45, Appl   |
| 14         | 11.4  | 39.3        | 65     | 4  | Sequence 37, Appl   |
| 15         | 11.2  | 38.6        | 25     | 1  | Sequence 28, Appl   |
| 16         | 11.2  | 38.6        | 25     | 1  | Sequence 28, Appl   |
| 17         | 11.2  | 38.6        | 25     | 2  | Sequence 28, Appl   |
| 18         | 11.2  | 38.6        | 25     | 3  | Sequence 28, Appl   |
| 19         | 11.2  | 38.6        | 25     | 3  | Sequence 28, Appl   |
| 20         | 11.2  | 38.6        | 25     | 4  | Sequence 28, Appl   |
| 21         | 11.2  | 38.6        | 33     | 1  | Sequence 29, Appl   |
| 22         | 11.2  | 38.6        | 33     | 1  | Sequence 29, Appl   |
| 23         | 11.2  | 38.6        | 33     | 2  | Sequence 29, Appl   |
| 24         | 11.2  | 38.6        | 33     | 3  | Sequence 29, Appl   |
| 25         | 11.2  | 38.6        | 33     | 3  | Sequence 29, Appl   |
| 26         | 11.2  | 38.6        | 33     | 3  | Sequence 29, Appl   |
| 27         | 11.2  | 38.6        | 33     | 4  | Sequence 29, Appl   |

|     |      |      |     |      |      |    |                    |                    |
|-----|------|------|-----|------|------|----|--------------------|--------------------|
| 33  | 38.6 | 11.2 | 28  | 11.2 | 38.6 | 4  | US-09-236-140A-29  | Sequence 29, Appl  |
| 36  | 38.6 | 11.2 | 29  | 11.2 | 38.6 | 2  | US-08-642-045B-17  | Sequence 17, Appl  |
| 36  | 38.6 | 11.2 | 30  | 11.2 | 38.6 | 3  | US-08-852-268-17   | Sequence 17, Appl  |
| 31  | 38.6 | 11.2 | 31  | 11.2 | 38.6 | 4  | US-09-571-774-2    | Sequence 2, Appl   |
| 41  | 38.6 | 11.2 | 32  | 11.2 | 38.6 | 4  | US-09-852-385-2    | Sequence 2, Appl   |
| 47  | 38.6 | 11.2 | 33  | 11.2 | 38.6 | 4  | US-09-422-978-2842 | Sequence 2842, Ap  |
| 52  | 38.6 | 11.2 | 34  | 11.2 | 38.6 | 4  | US-09-310-463-6    | Sequence 6, Appl   |
| 52  | 38.6 | 11.2 | 35  | 11.2 | 38.6 | 4  | US-08-842-248A-6   | Sequence 6, Appl   |
| 36  | 11.2 | 38.6 | 36  | 11.2 | 38.6 | 3  | US-09-364-380-29   | Sequence 29, Appl  |
| 31  | 37.9 | 11   | 37  | 11   | 37.9 | 31 | US-08-323-531-71   | Sequence 71, Appl  |
| 31  | 37.9 | 11   | 38  | 11   | 37.9 | 31 | US-08-198-094-71   | Sequence 71, Appl  |
| 31  | 37.9 | 11   | 39  | 11   | 37.9 | 31 | US-08-480-640A-119 | Sequence 119, Appl |
| 31  | 37.9 | 11   | 40  | 11   | 37.9 | 31 | US-08-295-802-119  | Sequence 119, Appl |
| 31  | 37.9 | 11   | 41  | 11   | 37.9 | 31 | US-08-107-794A-71  | Sequence 71, Appl  |
| 31  | 37.9 | 11   | 42  | 11   | 37.9 | 31 | US-08-488-237A-119 | Sequence 119, Appl |
| 31  | 37.9 | 11   | 43  | 11   | 37.9 | 31 | US-08-375-992A-119 | Sequence 119, Appl |
| 31  | 37.9 | 11   | 44  | 11   | 37.9 | 31 | US-08-472-679H-119 | Sequence 119, Appl |
| 31  | 37.9 | 11   | 45  | 11   | 37.9 | 31 | PCT-US93-07424-71  | Sequence 71, Appl  |
| 31  | 37.9 | 11   | 46  | 11   | 37.9 | 31 | PCT-US95-02087-71  | Sequence 71, Appl  |
| 34  | 37.9 | 11   | 47  | 11   | 37.9 | 34 | US-09-581-070-2    | Sequence 2, Appl   |
| 34  | 37.9 | 11   | 48  | 11   | 37.9 | 34 | US-09-581-070-5    | Sequence 5, Appl   |
| 70  | 37.9 | 11   | 49  | 11   | 37.9 | 70 | US-08-488-402A-127 | Sequence 127, Appl |
| 70  | 37.9 | 11   | 50  | 11   | 37.9 | 70 | US-08-484-552A-127 | Sequence 127, Appl |
| 70  | 37.9 | 11   | 51  | 11   | 37.9 | 70 | PCT-US96-09472-127 | Sequence 127, Appl |
| 19  | 37.2 | 10.8 | 52  | 10.8 | 37.2 | 19 | US-08-365-109B-3   | Sequence 3, Appl   |
| 19  | 37.2 | 10.8 | 53  | 10.8 | 37.2 | 19 | US-08-365-109B-3   | Sequence 3, Appl   |
| 20  | 37.2 | 10.8 | 54  | 10.8 | 37.2 | 20 | US-09-560-594-53   | Sequence 53, Appl  |
| 25  | 37.2 | 10.8 | 55  | 10.8 | 37.2 | 25 | US-08-943-731-336  | Sequence 336, Appl |
| 25  | 37.2 | 10.8 | 56  | 10.8 | 37.2 | 25 | US-09-827-998-1097 | Sequence 1097, Ap  |
| 25  | 37.2 | 10.8 | 57  | 10.8 | 37.2 | 25 | US-09-827-998-1098 | Sequence 1098, Ap  |
| 25  | 37.2 | 10.8 | 58  | 10.8 | 37.2 | 25 | US-09-827-998-1099 | Sequence 1099, Ap  |
| 25  | 37.2 | 10.8 | 59  | 10.8 | 37.2 | 25 | US-09-827-998-1100 | Sequence 1100, Ap  |
| 25  | 37.2 | 10.8 | 60  | 10.8 | 37.2 | 25 | US-09-827-998-1101 | Sequence 1101, Ap  |
| 25  | 37.2 | 10.8 | 61  | 10.8 | 37.2 | 25 | US-09-827-998-1102 | Sequence 1102, Ap  |
| 25  | 37.2 | 10.8 | 62  | 10.8 | 37.2 | 25 | US-09-827-998-1103 | Sequence 1103, Ap  |
| 25  | 37.2 | 10.8 | 63  | 10.8 | 37.2 | 25 | US-09-827-998-1104 | Sequence 1104, Ap  |
| 27  | 37.2 | 10.8 | 64  | 10.8 | 37.2 | 27 | US-09-253-396A-137 | Sequence 137, Appl |
| 29  | 37.2 | 10.8 | 65  | 10.8 | 37.2 | 29 | US-09-304-232-416  | Sequence 416, Appl |
| 45  | 37.2 | 10.8 | 66  | 10.8 | 37.2 | 45 | US-08-171-389-130  | Sequence 130, Appl |
| 45  | 37.2 | 10.8 | 67  | 10.8 | 37.2 | 45 | US-08-171-389-342  | Sequence 342, Appl |
| 45  | 37.2 | 10.8 | 68  | 10.8 | 37.2 | 45 | US-08-123-936-130  | Sequence 130, Appl |
| 45  | 37.2 | 10.8 | 69  | 10.8 | 37.2 | 45 | US-08-123-936-342  | Sequence 342, Appl |
| 45  | 37.2 | 10.8 | 70  | 10.8 | 37.2 | 45 | US-08-475-228A-130 | Sequence 130, Appl |
| 45  | 37.2 | 10.8 | 71  | 10.8 | 37.2 | 45 | US-08-475-228A-342 | Sequence 342, Appl |
| 45  | 37.2 | 10.8 | 72  | 10.8 | 37.2 | 45 | US-08-482-080A-130 | Sequence 130, Appl |
| 45  | 37.2 | 10.8 | 73  | 10.8 | 37.2 | 45 | US-08-482-080A-342 | Sequence 342, Appl |
| 45  | 37.2 | 10.8 | 74  | 10.8 | 37.2 | 45 | US-09-354-947-130  | Sequence 130, Appl |
| 45  | 37.2 | 10.8 | 75  | 10.8 | 37.2 | 45 | US-09-354-947-342  | Sequence 342, Appl |
| 45  | 37.2 | 10.8 | 76  | 10.8 | 37.2 | 45 | PCT-US93-12388-130 | Sequence 130, Appl |
| 45  | 37.2 | 10.8 | 77  | 10.8 | 37.2 | 45 | PCT-US93-12388-342 | Sequence 342, Appl |
| 47  | 37.2 | 10.8 | 78  | 10.8 | 37.2 | 47 | US-09-422-978-2286 | Sequence 2286, Ap  |
| 47  | 37.2 | 10.8 | 79  | 10.8 | 37.2 | 47 | US-09-422-978-3545 | Sequence 3545, Ap  |
| 48  | 37.2 | 10.8 | 80  | 10.8 | 37.2 | 48 | US-08-119-773-13   | Sequence 13, Appl  |
| 50  | 37.2 | 10.8 | 81  | 10.8 | 37.2 | 50 | US-08-171-389-343  | Sequence 343, Appl |
| 50  | 37.2 | 10.8 | 82  | 10.8 | 37.2 | 50 | US-08-123-936-343  | Sequence 343, Appl |
| 50  | 37.2 | 10.8 | 83  | 10.8 | 37.2 | 50 | US-08-633-368-3    | Sequence 3, Appl   |
| 50  | 37.2 | 10.8 | 84  | 10.8 | 37.2 | 50 | US-08-475-228A-343 | Sequence 343, Appl |
| 50  | 37.2 | 10.8 | 85  | 10.8 | 37.2 | 50 | US-08-482-080A-343 | Sequence 343, Appl |
| 50  | 37.2 | 10.8 | 86  | 10.8 | 37.2 | 50 | US-09-354-947-343  | Sequence 343, Appl |
| 50  | 37.2 | 10.8 | 87  | 10.8 | 37.2 | 50 | PCT-US93-12388-343 | Sequence 343, Appl |
| 51  | 37.2 | 10.8 | 88  | 10.8 | 37.2 | 51 | US-08-220-151-39   | Sequence 39, Appl  |
| 51  | 37.2 | 10.8 | 89  | 10.8 | 37.2 | 51 | US-08-413-118-39   | Sequence 39, Appl  |
| 51  | 37.2 | 10.8 | 90  | 10.8 | 37.2 | 51 | US-08-224-657-16   | Sequence 16, Appl  |
| 51  | 37.2 | 10.8 | 91  | 10.8 | 37.2 | 51 | US-08-257-073-83   | Sequence 83, Appl  |
| 51  | 37.2 | 10.8 | 92  | 10.8 | 37.2 | 51 | US-08-184-009-16   | Sequence 16, Appl  |
| 51  | 37.2 | 10.8 | 93  | 10.8 | 37.2 | 51 | US-08-486-969-16   | Sequence 16, Appl  |
| 51  | 37.2 | 10.8 | 94  | 10.8 | 37.2 | 51 | US-08-417-210A-16  | Sequence 16, Appl  |
| 51  | 37.2 | 10.8 | 95  | 10.8 | 37.2 | 51 | US-08-458-356-16   | Sequence 16, Appl  |
| 51  | 37.2 | 10.8 | 96  | 10.8 | 37.2 | 51 | US-08-471-025-16   | Sequence 16, Appl  |
| 51  | 37.2 | 10.8 | 97  | 10.8 | 37.2 | 51 | US-08-473-445-39   | Sequence 39, Appl  |
| 51  | 37.2 | 10.8 | 98  | 10.8 | 37.2 | 51 | US-08-460-736-16   | Sequence 16, Appl  |
| 51  | 37.2 | 10.8 | 99  | 10.8 | 37.2 | 51 | US-09-354-138-16   | Sequence 16, Appl  |
| 100 | 37.2 | 10.8 | 100 | 10.8 | 37.2 | 4  | US-09-535-370-16   | Sequence 16, Appl  |

|       |      |      |    |   |                     |                    |       |      |      |    |   |                     |                   |
|-------|------|------|----|---|---------------------|--------------------|-------|------|------|----|---|---------------------|-------------------|
| C 101 | 10.8 | 37.2 | 51 | 4 | US-09-136-159A-16   | Sequence 16, Appl  | C 174 | 10.2 | 35.2 | 45 | 1 | US-08-701-269-4     | Sequence 4, Appl  |
| C 102 | 10.8 | 37.2 | 51 | 5 | PCT-US96-00547-16   | Sequence 16, Appl  | C 175 | 10.2 | 35.2 | 45 | 2 | US-08-850-043-86    | Sequence 86, Appl |
| C 103 | 10.8 | 37.2 | 51 | 6 | US-08-956-171E-1736 | Sequence 1736, Ap  | C 176 | 10.2 | 35.2 | 45 | 3 | US-08-050-478-86    | Sequence 86, Appl |
| C 104 | 10.6 | 36.6 | 29 | 4 | US-09-304-232-644   | Sequence 644, App  | C 177 | 10.2 | 35.2 | 45 | 3 | US-09-414-117-86    | Sequence 86, Appl |
| C 105 | 10.6 | 36.6 | 30 | 2 | US-09-001-826-11    | Sequence 11, Appl  | C 178 | 10.2 | 35.2 | 45 | 4 | US-09-678-417-86    | Sequence 12, Appl |
| C 106 | 10.6 | 36.6 | 30 | 4 | US-09-561-825-7     | Sequence 7, Appl   | C 179 | 10.2 | 35.2 | 46 | 3 | US-09-171-878-12    | Sequence 12, Appl |
| C 107 | 10.6 | 36.6 | 30 | 4 | US-09-268-884-11    | Sequence 11, Appl  | C 180 | 10.2 | 35.2 | 46 | 4 | US-09-478-189-125   | Sequence 125, App |
| C 108 | 10.6 | 36.6 | 35 | 1 | US-08-497-312-8     | Sequence 8, Appl   | C 181 | 10.2 | 35.2 | 47 | 4 | US-09-422-978-686   | Sequence 686, App |
| C 109 | 10.6 | 36.6 | 36 | 1 | US-08-497-312-10    | Sequence 10, Appl  | C 182 | 10.2 | 35.2 | 47 | 4 | US-09-422-978-1097  | Sequence 1097, Ap |
| C 110 | 10.6 | 36.6 | 36 | 1 | US-09-242-913B-4    | Sequence 4, Appl   | C 183 | 10.2 | 35.2 | 47 | 4 | US-09-422-978-1171  | Sequence 1171, Ap |
| C 111 | 10.6 | 36.6 | 41 | 4 | US-09-666-890-1     | Sequence 2273, Ap  | C 184 | 10.2 | 35.2 | 48 | 1 | US-08-171-389-191   | Sequence 191, App |
| C 112 | 10.6 | 36.6 | 47 | 4 | US-09-422-978-2273  | Sequence 2273, Ap  | C 185 | 10.2 | 35.2 | 48 | 1 | US-08-123-936-191   | Sequence 191, App |
| C 113 | 10.6 | 36.6 | 50 | 2 | US-09-282-147-43    | Sequence 43, Appl  | C 186 | 10.2 | 35.2 | 48 | 3 | US-08-475-228A-191  | Sequence 191, App |
| C 114 | 10.6 | 36.6 | 54 | 2 | US-08-649-981-6     | Sequence 6, Appl   | C 187 | 10.2 | 35.2 | 48 | 3 | US-08-482-080A-191  | Sequence 191, App |
| C 115 | 10.6 | 36.6 | 60 | 1 | US-08-256-964A-7    | Sequence 7, Appl   | C 188 | 10.2 | 35.2 | 48 | 4 | US-09-354-947-191   | Sequence 191, App |
| C 116 | 10.6 | 36.6 | 60 | 3 | US-08-483-511-77    | Sequence 77, Appl  | C 189 | 10.2 | 35.2 | 48 | 5 | PCT-US93-12388-191  | Sequence 191, App |
| C 117 | 10.4 | 35.9 | 20 | 4 | US-09-422-978-5557  | Sequence 5557, Ap  | C 190 | 10.2 | 35.2 | 50 | 1 | US-08-036-217-19    | Sequence 19, Appl |
| C 118 | 10.4 | 35.9 | 20 | 4 | US-09-909-595-40    | Sequence 40, Appl  | C 191 | 10.2 | 35.2 | 50 | 1 | US-08-105-483-19    | Sequence 19, Appl |
| C 119 | 10.4 | 35.9 | 26 | 1 | US-08-599-252-43    | Sequence 43, Appl  | C 192 | 10.2 | 35.2 | 50 | 1 | US-08-073-963-35    | Sequence 35, Appl |
| C 120 | 10.4 | 35.9 | 26 | 5 | PCT-US96-06352-43   | Sequence 43, Appl  | C 193 | 10.2 | 35.2 | 50 | 1 | US-07-714-687-19    | Sequence 19, Appl |
| C 121 | 10.4 | 35.9 | 26 | 5 | PCT-US96-06583-43   | Sequence 43, Appl  | C 194 | 10.2 | 35.2 | 50 | 1 | US-08-220-151-42    | Sequence 42, Appl |
| C 122 | 10.4 | 35.9 | 27 | 2 | US-08-724-354D-19   | Sequence 19, Appl  | C 195 | 10.2 | 35.2 | 50 | 1 | US-08-171-389-466   | Sequence 466, App |
| C 123 | 10.4 | 35.9 | 29 | 3 | US-09-270-984A-19   | Sequence 19, Appl  | C 196 | 10.2 | 35.2 | 50 | 1 | US-08-413-118-42    | Sequence 42, Appl |
| C 124 | 10.4 | 35.9 | 29 | 3 | US-08-761-277A-77   | Sequence 77, Appl  | C 197 | 10.2 | 35.2 | 50 | 1 | US-08-123-936-466   | Sequence 466, App |
| C 125 | 10.4 | 35.9 | 40 | 4 | US-09-731-466-1     | Sequence 1, Appl   | C 198 | 10.2 | 35.2 | 50 | 1 | US-08-224-391-19    | Sequence 19, Appl |
| C 126 | 10.4 | 35.9 | 41 | 2 | US-08-833-814A-6    | Sequence 6, Appl   | C 199 | 10.2 | 35.2 | 50 | 1 | US-08-484-304-19    | Sequence 19, Appl |
| C 127 | 10.4 | 35.9 | 47 | 4 | US-09-422-978-133   | Sequence 133, App  | C 200 | 10.2 | 35.2 | 50 | 1 | US-08-224-657-19    | Sequence 19, Appl |
| C 128 | 10.4 | 35.9 | 47 | 4 | US-09-422-978-430   | Sequence 430, App  | C 201 | 10.2 | 35.2 | 50 | 1 | US-08-475-063-19    | Sequence 19, Appl |
| C 129 | 10.4 | 35.9 | 47 | 4 | US-09-422-978-734   | Sequence 734, App  | C 202 | 10.2 | 35.2 | 50 | 1 | US-08-207-793-19    | Sequence 19, Appl |
| C 130 | 10.4 | 35.9 | 47 | 4 | US-09-422-978-2892  | Sequence 2892, Ap  | C 203 | 10.2 | 35.2 | 50 | 1 | US-08-487-412-35    | Sequence 35, Appl |
| C 131 | 10.4 | 35.9 | 47 | 4 | US-09-422-978-3619  | Sequence 3619, Ap  | C 204 | 10.2 | 35.2 | 50 | 1 | US-08-709-209-19    | Sequence 19, Appl |
| C 132 | 10.4 | 35.9 | 49 | 3 | US-09-522-494-47    | Sequence 47, Appl  | C 205 | 10.2 | 35.2 | 50 | 1 | US-08-257-073-86    | Sequence 86, Appl |
| C 133 | 10.4 | 35.9 | 49 | 4 | US-09-428-082B-401  | Sequence 401, App  | C 206 | 10.2 | 35.2 | 50 | 1 | US-08-303-275-19    | Sequence 19, Appl |
| C 134 | 10.4 | 35.9 | 55 | 4 | US-09-621-976-18457 | Sequence 18457, A  | C 207 | 10.2 | 35.2 | 50 | 2 | US-08-458-101-19    | Sequence 19, Appl |
| C 135 | 10.4 | 35.9 | 57 | 4 | US-09-428-082B-415  | Sequence 415, App  | C 208 | 10.2 | 35.2 | 50 | 2 | US-08-486-969-19    | Sequence 19, Appl |
| C 136 | 10.4 | 35.9 | 60 | 4 | US-09-428-082B-415  | Sequence 415, App  | C 209 | 10.2 | 35.2 | 50 | 2 | US-08-475-228A-466  | Sequence 466, App |
| C 137 | 10.4 | 35.9 | 61 | 4 | US-09-428-082B-400  | Sequence 400, App  | C 210 | 10.2 | 35.2 | 50 | 2 | US-08-458-356-19    | Sequence 19, Appl |
| C 138 | 10.4 | 35.9 | 70 | 3 | US-09-364-380-31    | Sequence 31, Appl  | C 211 | 10.2 | 35.2 | 50 | 2 | US-08-471-025-19    | Sequence 19, Appl |
| C 139 | 10.4 | 35.9 | 71 | 2 | US-08-465-591A-57   | Sequence 57, Appl  | C 212 | 10.2 | 35.2 | 50 | 2 | US-08-658-665-19    | Sequence 19, Appl |
| C 140 | 10.4 | 35.9 | 71 | 2 | US-08-465-594A-57   | Sequence 57, Appl  | C 213 | 10.2 | 35.2 | 50 | 2 | US-08-482-080A-466  | Sequence 466, App |
| C 141 | 10.4 | 35.9 | 71 | 5 | US-08-973-124-242   | Sequence 242, App  | C 214 | 10.2 | 35.2 | 50 | 3 | US-08-473-446-42    | Sequence 42, Appl |
| C 142 | 10.4 | 35.9 | 71 | 5 | PCT-US96-08014-242  | Sequence 242, App  | C 215 | 10.2 | 35.2 | 50 | 3 | US-08-460-736-19    | Sequence 19, Appl |
| C 143 | 10.4 | 35.9 | 77 | 6 | 5182195-3           | Patent No. 5182195 | C 216 | 10.2 | 35.2 | 50 | 3 | US-09-085-273-19    | Sequence 19, Appl |
| C 144 | 10.4 | 35.9 | 78 | 6 | 5182195-6           | Patent No. 5182195 | C 217 | 10.2 | 35.2 | 50 | 3 | US-09-085-273-19    | Sequence 19, Appl |
| C 145 | 10.2 | 35.2 | 20 | 3 | US-09-407-818-15    | Sequence 15, Appl  | C 218 | 10.2 | 35.2 | 50 | 4 | US-09-354-947-466   | Sequence 466, App |
| C 146 | 10.2 | 35.2 | 20 | 4 | US-09-853-768-51    | Sequence 51, Appl  | C 219 | 10.2 | 35.2 | 50 | 4 | US-09-354-947-466   | Sequence 466, App |
| C 147 | 10.2 | 35.2 | 21 | 2 | US-08-797-689-20    | Sequence 20, Appl  | C 220 | 10.2 | 35.2 | 50 | 4 | US-09-535-370-19    | Sequence 19, Appl |
| C 148 | 10.2 | 35.2 | 21 | 4 | US-09-422-978-11708 | Sequence 11708, A  | C 221 | 10.2 | 35.2 | 50 | 4 | US-09-136-159A-19   | Sequence 19, Appl |
| C 149 | 10.2 | 35.2 | 21 | 4 | US-09-984-186-20    | Sequence 20, Appl  | C 222 | 10.2 | 35.2 | 50 | 4 | US-09-916-963-19    | Sequence 19, Appl |
| C 150 | 10.2 | 35.2 | 22 | 2 | US-08-474-450A-17   | Sequence 17, Appl  | C 223 | 10.2 | 35.2 | 50 | 4 | PCT-US93-12388-466  | Sequence 466, App |
| C 151 | 10.2 | 35.2 | 22 | 4 | US-08-983-466-48    | Sequence 48, Appl  | C 224 | 10.2 | 35.2 | 50 | 5 | PCT-US96-00547-19   | Sequence 19, Appl |
| C 152 | 10.2 | 35.2 | 24 | 4 | US-09-085-686-4     | Sequence 4, Appl   | C 225 | 10.2 | 35.2 | 50 | 5 | US-09-443-139C-306  | Sequence 306, App |
| C 153 | 10.2 | 35.2 | 29 | 2 | US-08-716-317-25    | Sequence 25, Appl  | C 226 | 10.2 | 35.2 | 51 | 4 | US-09-037-9908-47   | Sequence 47, Appl |
| C 154 | 10.2 | 35.2 | 30 | 1 | US-08-479-487-13    | Sequence 13, Appl  | C 227 | 10.2 | 35.2 | 56 | 3 | US-08-842-842-5     | Sequence 5, Appl  |
| C 155 | 10.2 | 35.2 | 30 | 2 | US-08-621-564B-4    | Sequence 4, Appl   | C 228 | 10.2 | 35.2 | 59 | 2 | US-09-052-521C-25   | Sequence 25, Appl |
| C 156 | 10.2 | 35.2 | 30 | 3 | US-08-621-841-51    | Sequence 51, Appl  | C 229 | 10.2 | 35.2 | 59 | 4 | US-09-126-640-38    | Sequence 38, Appl |
| C 157 | 10.2 | 35.2 | 30 | 3 | US-09-269-220-4     | Sequence 4, Appl   | C 230 | 10.2 | 35.2 | 60 | 3 | US-09-288-292A-38   | Sequence 38, Appl |
| C 158 | 10.2 | 35.2 | 31 | 1 | US-07-977-284A-233  | Sequence 233, App  | C 231 | 10.2 | 35.2 | 60 | 4 | US-08-966-171B-3478 | Sequence 3478, Ap |
| C 159 | 10.2 | 35.2 | 31 | 1 | US-08-256-426B-233  | Sequence 233, App  | C 232 | 10.2 | 35.2 | 60 | 4 | US-08-926-246-38    | Sequence 38, Appl |
| C 160 | 10.2 | 35.2 | 33 | 1 | US-08-153-848-63    | Sequence 63, App   | C 233 | 10.2 | 35.2 | 64 | 3 | US-08-944-495-38    | Sequence 38, Appl |
| C 161 | 10.2 | 35.2 | 33 | 1 | US-08-372-652-11    | Sequence 11, Appl  | C 234 | 10.2 | 35.2 | 64 | 3 | US-08-925-588-38    | Sequence 38, Appl |
| C 162 | 10.2 | 35.2 | 33 | 4 | US-09-299-843A-63   | Sequence 63, Appl  | C 235 | 10.2 | 35.2 | 64 | 4 | US-09-372-044-38    | Sequence 38, Appl |
| C 163 | 10.2 | 35.2 | 33 | 4 | US-09-088-332B-63   | Sequence 63, Appl  | C 236 | 10.2 | 35.2 | 64 | 4 | US-08-825-486-38    | Sequence 38, Appl |
| C 164 | 10.2 | 35.2 | 33 | 5 | PCT-US93-11153-63   | Sequence 63, Appl  | C 237 | 10.2 | 35.2 | 65 | 4 | US-09-052-521C-23   | Sequence 23, Appl |
| C 165 | 10.2 | 35.2 | 33 | 5 | PCT-US95-16311-11   | Sequence 11, Appl  | C 238 | 10.2 | 35.2 | 66 | 4 | US-08-956-171B-3478 | Sequence 3478, Ap |
| C 166 | 10.2 | 35.2 | 34 | 2 | US-08-455-968B-50   | Sequence 50, Appl  | C 239 | 10.2 | 35.2 | 66 | 4 | US-08-275-850-121   | Sequence 121, App |
| C 167 | 10.2 | 35.2 | 35 | 1 | US-08-297-706-4     | Sequence 4, Appl   | C 240 | 10.2 | 35.2 | 68 | 3 | US-08-105-483-449   | Sequence 449, App |
| C 168 | 10.2 | 35.2 | 35 | 5 | PCT-US93-05759-4    | Sequence 4, Appl   | C 241 | 10.2 | 35.2 | 70 | 1 | US-08-709-209-449   | Sequence 449, App |
| C 169 | 10.2 | 35.2 | 38 | 3 | US-08-844-274-22    | Sequence 22, Appl  | C 242 | 10.2 | 35.2 | 70 | 1 | US-08-303-275-161   | Sequence 161, App |
| C 170 | 10.2 | 35.2 | 38 | 4 | US-09-598-421-22    | Sequence 22, Appl  | C 243 | 10.2 | 35.2 | 70 | 1 | US-08-458-101-449   | Sequence 449, App |
| C 171 | 10.2 | 35.2 | 42 | 2 | US-08-840-887-4     | Sequence 4, Appl   | C 244 | 10.2 | 35.2 | 70 | 2 | US-08-488-402A-157  | Sequence 157, App |
| C 172 | 10.2 | 35.2 | 42 | 4 | US-10-077-480-5     | Sequence 5, Appl   | C 245 | 10.2 | 35.2 | 70 | 2 | US-08-484-552A-157  | Sequence 157, App |
| C 173 | 10.2 | 35.2 | 45 | 1 | US-08-229-279-4     | Sequence 4, Appl   | C 246 | 10.2 | 35.2 | 70 | 2 |                     |                   |

|       |      |      |    |   |                     |                    |       |     |      |    |   |                      |                    |
|-------|------|------|----|---|---------------------|--------------------|-------|-----|------|----|---|----------------------|--------------------|
| 247   | 10.2 | 35.2 | 70 | 5 | PCT-US96-09472-157  | Sequence 157, App  | 320   | 10  | 34.5 | 47 | 4 | US-09-422-978-1676   | Sequence 1676, Ap  |
| C 248 | 10.2 | 35.2 | 71 | 1 | US-08-472-255A-108  | Sequence 108, App  | C 321 | 10  | 34.5 | 47 | 4 | US-09-422-978-2668   | Sequence 2668, Ap  |
| C 249 | 10.2 | 35.2 | 71 | 1 | US-08-479-724A-108  | Sequence 108, App  | C 322 | 10  | 34.5 | 47 | 4 | US-09-422-978-2903   | Sequence 2903, Ap  |
| C 250 | 10.2 | 35.2 | 71 | 3 | US-08-472-256B-108  | Sequence 108, App  | C 323 | 10  | 34.5 | 48 | 6 | 5240845-53           | Patent No. 5240845 |
| C 251 | 10.2 | 35.2 | 71 | 3 | US-08-472-256B-108  | Sequence 108, App  | C 324 | 10  | 34.5 | 49 | 3 | US-09-522-494-46     | Sequence 46, Appl  |
| C 252 | 10.2 | 35.2 | 71 | 4 | US-08-482-793-108   | Sequence 108, App  | C 325 | 10  | 34.5 | 50 | 2 | US-08-472-171-27     | Sequence 27, Appl  |
| C 253 | 10.2 | 35.2 | 71 | 4 | US-08-482-793-108   | Sequence 108, App  | C 326 | 10  | 34.5 | 50 | 2 | US-08-484-526-27     | Sequence 27, Appl  |
| C 254 | 10.2 | 35.2 | 80 | 4 | PCT-US96-09455A-108 | Sequence 108, App  | C 327 | 10  | 34.5 | 50 | 2 | US-08-013-047-27     | Sequence 27, Appl  |
| 255   | 10   | 34.5 | 16 | 4 | US-09-397-168-47    | Sequence 32, Appl  | C 328 | 10  | 34.5 | 50 | 3 | US-09-374-597-27     | Sequence 27, Appl  |
| 256   | 10   | 34.5 | 19 | 4 | US-09-422-978-6220  | Sequence 6220, App | C 329 | 10  | 34.5 | 50 | 4 | US-08-956-171E-2247  | Sequence 2247, Ap  |
| C 257 | 10   | 34.5 | 20 | 1 | US-08-249-386A-2    | Sequence 2, Appl   | 330   | 10  | 34.5 | 50 | 6 | 5240845-44           | Patent No. 5240845 |
| C 258 | 10   | 34.5 | 20 | 1 | US-08-249-386A-10   | Sequence 10, Appl  | C 331 | 10  | 34.5 | 53 | 3 | US-08-864-473-62     | Sequence 62, Appl  |
| C 259 | 10   | 34.5 | 20 | 1 | US-08-227-180B-27   | Sequence 27, Appl  | C 332 | 10  | 34.5 | 53 | 3 | US-09-440-523-62     | Sequence 62, Appl  |
| 260   | 10   | 34.5 | 20 | 3 | US-09-488-857B-34   | Sequence 34, Appl  | C 333 | 10  | 34.5 | 57 | 2 | US-08-663-566A-55    | Sequence 55, Appl  |
| C 261 | 10   | 34.5 | 20 | 4 | US-09-710-200-12    | Sequence 12, Appl  | C 334 | 10  | 34.5 | 57 | 2 | US-08-288-065A-55    | Sequence 55, Appl  |
| C 262 | 10   | 34.5 | 20 | 4 | US-09-331-359-6     | Sequence 6, Appl   | C 335 | 10  | 34.5 | 57 | 2 | US-08-362-240A-55    | Sequence 55, Appl  |
| C 263 | 10   | 34.5 | 20 | 4 | US-09-975-408-12    | Sequence 12, Appl  | C 336 | 10  | 34.5 | 57 | 3 | US-08-804-372A-17    | Sequence 17, Appl  |
| C 264 | 10   | 34.5 | 20 | 5 | PCT-US95-06160-2    | Sequence 2, Appl   | C 337 | 10  | 34.5 | 57 | 5 | PCT-US95-10245-55    | Sequence 55, Appl  |
| C 265 | 10   | 34.5 | 20 | 5 | PCT-US95-06160-10   | Sequence 10, Appl  | C 338 | 10  | 34.5 | 61 | 4 | US-09-549-848B-66    | Sequence 66, Appl  |
| C 266 | 10   | 34.5 | 21 | 4 | US-09-337-168-48    | Sequence 48, Appl  | C 339 | 10  | 34.5 | 65 | 4 | US-09-495-050A-258   | Sequence 258, App  |
| C 267 | 10   | 34.5 | 22 | 4 | US-09-322-409-131   | Sequence 131, App  | C 340 | 10  | 34.5 | 75 | 1 | US-07-971-101-6      | Sequence 6, Appl   |
| C 268 | 10   | 34.5 | 22 | 4 | US-09-451-527-131   | Sequence 131, App  | C 341 | 9.8 | 33.8 | 16 | 6 | 5171843-4            | Patent No. 5171843 |
| C 269 | 10   | 34.5 | 24 | 3 | US-09-522-494-49    | Sequence 49, App   | C 342 | 9.8 | 33.8 | 17 | 3 | US-08-998-099-58     | Sequence 58, Appl  |
| C 270 | 10   | 34.5 | 24 | 3 | US-09-522-494-49    | Sequence 50, App   | C 343 | 9.8 | 33.8 | 17 | 3 | US-08-998-099-59     | Sequence 59, Appl  |
| C 271 | 10   | 34.5 | 24 | 3 | US-09-522-494-51    | Sequence 51, App   | C 344 | 9.8 | 33.8 | 17 | 4 | US-09-827-998-281    | Sequence 281, App  |
| C 272 | 10   | 34.5 | 24 | 3 | US-09-522-494-52    | Sequence 52, App   | C 345 | 9.8 | 33.8 | 17 | 4 | US-09-827-998-282    | Sequence 282, App  |
| C 273 | 10   | 34.5 | 24 | 4 | US-08-011-336-9     | Sequence 9, Appl   | C 346 | 9.8 | 33.8 | 17 | 4 | US-09-827-998-283    | Sequence 283, App  |
| C 274 | 10   | 34.5 | 25 | 2 | US-08-690-734A-54   | Sequence 54, Appl  | C 347 | 9.8 | 33.8 | 17 | 4 | US-09-866-108A-10208 | Sequence 10208, A  |
| C 275 | 10   | 34.5 | 25 | 3 | US-08-742-185-54    | Sequence 54, Appl  | C 348 | 9.8 | 33.8 | 17 | 4 | US-09-866-108A-10209 | Sequence 10209, A  |
| C 276 | 10   | 34.5 | 25 | 4 | US-09-907-794A-321  | Sequence 321, App  | C 349 | 9.8 | 33.8 | 18 | 1 | US-08-119-773-15     | Sequence 15, Appl  |
| C 277 | 10   | 34.5 | 25 | 4 | US-09-905-125A-321  | Sequence 321, App  | C 350 | 9.8 | 33.8 | 18 | 4 | US-09-422-978-5466   | Sequence 5466, Ap  |
| C 278 | 10   | 34.5 | 25 | 4 | US-09-902-775A-321  | Sequence 321, App  | C 351 | 9.8 | 33.8 | 18 | 4 | US-09-422-978-7686   | Sequence 7686, Ap  |
| C 279 | 10   | 34.5 | 25 | 4 | US-08-279-058B-42   | Sequence 42, Appl  | C 352 | 9.8 | 33.8 | 19 | 3 | US-08-946-732-7      | Sequence 7, Appl   |
| C 280 | 10   | 34.5 | 27 | 1 | US-08-974-022-37    | Sequence 37, Appl  | C 353 | 9.8 | 33.8 | 19 | 3 | US-09-397-915-7      | Sequence 7, Appl   |
| C 281 | 10   | 34.5 | 27 | 3 | US-08-795-445A-37   | Sequence 37, Appl  | C 354 | 9.8 | 33.8 | 19 | 4 | US-09-422-978-4780   | Sequence 4780, Ap  |
| C 282 | 10   | 34.5 | 27 | 3 | US-08-795-447A-37   | Sequence 37, Appl  | C 355 | 9.8 | 33.8 | 19 | 4 | US-09-422-978-5884   | Sequence 5884, Ap  |
| C 283 | 10   | 34.5 | 27 | 3 | US-08-974-186-37    | Sequence 37, Appl  | C 356 | 9.8 | 33.8 | 19 | 4 | US-09-911-226-7      | Sequence 7, Appl   |
| C 284 | 10   | 34.5 | 27 | 3 | US-08-795-446B-37   | Sequence 37, Appl  | C 357 | 9.8 | 33.8 | 20 | 1 | US-08-555-394-9      | Sequence 9, Appl   |
| C 285 | 10   | 34.5 | 27 | 4 | US-08-706-945D-60   | Sequence 60, Appl  | C 358 | 9.8 | 33.8 | 20 | 2 | US-09-258-371-18     | Sequence 18, Appl  |
| C 286 | 10   | 34.5 | 27 | 4 | US-08-828-323-42    | Sequence 42, Appl  | C 359 | 9.8 | 33.8 | 20 | 3 | US-08-745-892-9      | Sequence 9, Appl   |
| C 287 | 10   | 34.5 | 27 | 4 | US-08-577-788C-37   | Sequence 37, Appl  | C 360 | 9.8 | 33.8 | 20 | 3 | US-08-751-230-18     | Sequence 18, Appl  |
| C 288 | 10   | 34.5 | 27 | 4 | US-10-112-602-16    | Sequence 16, Appl  | C 361 | 9.8 | 33.8 | 20 | 3 | US-09-150-805-10     | Sequence 10, Appl  |
| C 289 | 10   | 34.5 | 28 | 4 | US-08-281-495-57    | Sequence 57, Appl  | C 362 | 9.8 | 33.8 | 20 | 3 | US-09-499-082-18     | Sequence 18, Appl  |
| C 290 | 10   | 34.5 | 29 | 4 | US-09-020-846-7     | Sequence 7, Appl   | C 363 | 9.8 | 33.8 | 20 | 3 | US-09-025-151-3      | Sequence 3, Appl   |
| C 291 | 10   | 34.5 | 30 | 1 | US-07-940-605A-14   | Sequence 14, Appl  | C 364 | 9.8 | 33.8 | 20 | 3 | US-08-996-069A-10    | Sequence 10, Appl  |
| C 292 | 10   | 34.5 | 30 | 2 | US-08-690-096-14    | Sequence 14, Appl  | C 365 | 9.8 | 33.8 | 20 | 3 | US-09-258-372-18     | Sequence 18, Appl  |
| C 293 | 10   | 34.5 | 31 | 2 | US-08-487-753-16    | Sequence 16, Appl  | C 366 | 9.8 | 33.8 | 20 | 4 | US-09-689-255C-18    | Sequence 18, Appl  |
| C 294 | 10   | 34.5 | 31 | 2 | US-08-480-065-16    | Sequence 16, Appl  | C 367 | 9.8 | 33.8 | 20 | 4 | US-09-637-240-3      | Sequence 3, Appl   |
| C 295 | 10   | 34.5 | 31 | 3 | US-08-487-744-16    | Sequence 25, Appl  | C 368 | 9.8 | 33.8 | 20 | 4 | US-09-198-452A-3600  | Sequence 3600, Ap  |
| C 296 | 10   | 34.5 | 31 | 4 | US-09-232-225-25    | Sequence 25, Appl  | C 369 | 9.8 | 33.8 | 21 | 4 | US-09-564-805-153    | Sequence 153, App  |
| C 297 | 10   | 34.5 | 33 | 1 | US-08-667-079B-5    | Sequence 7, Appl   | C 370 | 9.8 | 33.8 | 21 | 4 | US-09-395-345-3      | Sequence 3, Appl   |
| C 298 | 10   | 34.5 | 33 | 4 | US-09-784-508-7     | Sequence 7, Appl   | C 371 | 9.8 | 33.8 | 21 | 6 | 5171843-13           | Patent No. 5171843 |
| C 299 | 10   | 34.5 | 35 | 2 | US-08-249-189-19    | Sequence 19, Appl  | C 372 | 9.8 | 33.8 | 22 | 3 | US-08-969-317-9      | Sequence 9, Appl   |
| C 300 | 10   | 34.5 | 35 | 2 | US-08-484-624A-19   | Sequence 19, Appl  | C 373 | 9.8 | 33.8 | 22 | 4 | US-09-159-871-10     | Sequence 10, Appl  |
| C 301 | 10   | 34.5 | 35 | 2 | US-08-477-733B-19   | Sequence 19, Appl  | C 374 | 9.8 | 33.8 | 22 | 4 | US-09-375-673B-49    | Sequence 49, Appl  |
| C 302 | 10   | 34.5 | 35 | 3 | US-08-088-913A-19   | Sequence 19, Appl  | C 375 | 9.8 | 33.8 | 23 | 2 | US-08-747-536-28     | Sequence 28, Appl  |
| C 303 | 10   | 34.5 | 35 | 3 | US-08-769-819-19    | Sequence 19, Appl  | C 376 | 9.8 | 33.8 | 23 | 4 | US-09-470-661A-22    | Sequence 22, Appl  |
| C 304 | 10   | 34.5 | 35 | 3 | US-08-770-974-19    | Sequence 19, Appl  | C 377 | 9.8 | 33.8 | 24 | 1 | US-08-287-442-7      | Sequence 7, Appl   |
| C 305 | 10   | 34.5 | 35 | 4 | US-08-770-981-19    | Sequence 19, Appl  | C 378 | 9.8 | 33.8 | 24 | 1 | US-08-459-701-7      | Sequence 7, Appl   |
| C 306 | 10   | 34.5 | 35 | 4 | US-09-399-106-19    | Sequence 19, Appl  | C 379 | 9.8 | 33.8 | 24 | 1 | US-08-460-298-7      | Sequence 7, Appl   |
| C 307 | 10   | 34.5 | 35 | 4 | US-09-539-333D-53   | Sequence 53, Appl  | C 380 | 9.8 | 33.8 | 24 | 2 | US-08-459-174-7      | Sequence 7, Appl   |
| C 308 | 10   | 34.5 | 36 | 4 | US-08-479-005A-809  | Sequence 809, App  | C 381 | 9.8 | 33.8 | 24 | 2 | US-08-592-383-10     | Sequence 10, Appl  |
| C 309 | 10   | 34.5 | 37 | 4 | US-08-479-005A-1131 | Sequence 1131, App | C 382 | 9.8 | 33.8 | 24 | 2 | US-08-332-766A-99    | Sequence 99, Appl  |
| C 310 | 10   | 34.5 | 38 | 1 | US-08-373-124A-809  | Sequence 809, App  | C 383 | 9.8 | 33.8 | 24 | 3 | US-08-751-512-2      | Sequence 2, Appl   |
| C 311 | 10   | 34.5 | 38 | 1 | US-08-435-628-809   | Sequence 809, App  | C 384 | 9.8 | 33.8 | 24 | 3 | US-08-641-291A-53    | Sequence 53, Appl  |
| C 312 | 10   | 34.5 | 38 | 4 | US-08-706-945D-66   | Sequence 66, Appl  | C 385 | 9.8 | 33.8 | 24 | 3 | US-08-641-291A-56    | Sequence 56, Appl  |
| C 313 | 10   | 34.5 | 40 | 2 | US-08-896-116-7     | Sequence 7, Appl   | C 386 | 9.8 | 33.8 | 25 | 3 | PCT-US93-06300A-7    | Sequence 7, Appl   |
| C 314 | 10   | 34.5 | 40 | 3 | US-08-896-122-7     | Sequence 7, Appl   | C 387 | 9.8 | 33.8 | 25 | 3 | US-08-945-056-18     | Sequence 18, Appl  |
| C 315 | 10   | 34.5 | 40 | 5 | PCT-US95-08487-7    | Sequence 7, Appl   | C 388 | 9.8 | 33.8 | 25 | 4 | US-09-827-998-1096   | Sequence 1096, Ap  |
| C 316 | 10   | 34.5 | 42 | 4 | US-10-037-927B-48   | Sequence 48, Appl  | C 389 | 9.8 | 33.8 | 25 | 4 | US-09-827-998-1105   | Sequence 1105, Ap  |
| C 317 | 10   | 34.5 | 42 | 4 | US-09-462-941-39    | Sequence 39, Appl  | C 390 | 9.8 | 33.8 | 25 | 4 | US-09-827-998-1106   | Sequence 1106, Ap  |
| C 318 | 10   | 34.5 | 45 | 4 | US-09-291-874-11    | Sequence 11, Appl  | C 391 | 9.8 | 33.8 | 25 | 4 | US-09-866-108A-15100 | Sequence 15100, A  |
| C 319 | 10   | 34.5 | 45 | 4 | US-09-344-783C-28   | Sequence 28, Appl  | C 392 | 9.8 | 33.8 | 25 | 4 | US-09-866-108A-15101 | Sequence 15101, A  |



|     |     |      |    |   |                      |                    |       |     |      |    |   |                    |                    |
|-----|-----|------|----|---|----------------------|--------------------|-------|-----|------|----|---|--------------------|--------------------|
| 393 | 9.8 | 33.8 | 25 | 4 | US-09-866-108A-15102 | Sequence 15102, A  | C 466 | 9.8 | 33.8 | 43 | 3 | US-09-150-805-7    | Sequence 7, Appli  |
| 394 | 9.8 | 33.8 | 25 | 4 | US-09-866-108A-15103 | Sequence 15103, A  | C 467 | 9.8 | 33.8 | 43 | 3 | US-08-996-069A-5   | Sequence 5, Appli  |
| 395 | 9.8 | 33.8 | 25 | 4 | US-09-866-108A-15104 | Sequence 15104, A  | C 468 | 9.8 | 33.8 | 43 | 3 | US-08-996-069A-7   | Sequence 7, Appli  |
| 396 | 9.8 | 33.8 | 25 | 4 | US-09-866-108A-15105 | Sequence 15105, A  | C 469 | 9.8 | 33.8 | 43 | 4 | US-09-434-354-4    | Sequence 4, Appli  |
| 397 | 9.8 | 33.8 | 25 | 4 | US-09-866-108A-15106 | Sequence 15106, A  | C 470 | 9.8 | 33.8 | 44 | 1 | US-07-832-905B-58  | Sequence 58, Appli |
| 398 | 9.8 | 33.8 | 25 | 4 | US-09-866-108A-15107 | Sequence 15107, A  | C 471 | 9.8 | 33.8 | 44 | 3 | US-08-700-757-58   | Sequence 58, Appli |
| 399 | 9.8 | 33.8 | 25 | 4 | US-09-866-108A-15108 | Sequence 15108, A  | C 472 | 9.8 | 33.8 | 44 | 3 | US-09-100-193-5    | Sequence 5, Appli  |
| 400 | 9.8 | 33.8 | 25 | 4 | US-09-866-108A-15109 | Sequence 15109, A  | C 473 | 9.8 | 33.8 | 47 | 1 | US-08-171-389-121  | Sequence 121, App  |
| 401 | 9.8 | 33.8 | 26 | 1 | US-08-458-023B-9     | Sequence 9, Appli  | C 474 | 9.8 | 33.8 | 47 | 1 | US-08-123-935-121  | Sequence 121, App  |
| 402 | 9.8 | 33.8 | 26 | 1 | US-08-445-746-12     | Sequence 12, Appli | C 475 | 9.8 | 33.8 | 47 | 2 | US-08-475-228A-121 | Sequence 121, App  |
| 403 | 9.8 | 33.8 | 26 | 3 | US-09-008-722-12     | Sequence 12, Appli | C 476 | 9.8 | 33.8 | 47 | 2 | US-08-700-670A-28  | Sequence 28, Appli |
| 404 | 9.8 | 33.8 | 26 | 4 | US-09-197-814-5      | Sequence 5, Appli  | C 477 | 9.8 | 33.8 | 47 | 2 | US-08-482-080A-121 | Sequence 121, App  |
| 405 | 9.8 | 33.8 | 26 | 4 | US-09-689-255C-6     | Sequence 6, Appli  | C 478 | 9.8 | 33.8 | 47 | 4 | US-09-354-947-121  | Sequence 121, App  |
| 406 | 9.8 | 33.8 | 26 | 4 | US-09-218-446-5      | Sequence 5, Appli  | C 479 | 9.8 | 33.8 | 47 | 4 | US-09-641-638-1124 | Sequence 1124, App |
| 407 | 9.8 | 33.8 | 26 | 4 | US-09-920-591-5      | Sequence 5, Appli  | C 480 | 9.8 | 33.8 | 47 | 4 | US-09-671-317-500  | Sequence 500, Appl |
| 408 | 9.8 | 33.8 | 26 | 4 | US-09-068-357-13     | Sequence 13, Appli | C 481 | 9.8 | 33.8 | 47 | 4 | US-09-422-978-56   | Sequence 56, Appl  |
| 409 | 9.8 | 33.8 | 27 | 1 | US-08-117-364A-12    | Sequence 12, Appli | C 482 | 9.8 | 33.8 | 47 | 4 | US-09-422-978-1012 | Sequence 1012, Ap  |
| 410 | 9.8 | 33.8 | 27 | 1 | US-08-458-489-5      | Sequence 5, Appli  | C 483 | 9.8 | 33.8 | 47 | 4 | US-09-422-978-1306 | Sequence 1306, Ap  |
| 411 | 9.8 | 33.8 | 27 | 1 | US-08-458-489-5      | Sequence 5, Appli  | C 484 | 9.8 | 33.8 | 47 | 4 | US-09-422-978-2469 | Sequence 2469, Ap  |
| 412 | 9.8 | 33.8 | 27 | 1 | US-07-843-350C-5     | Sequence 5, Appli  | C 485 | 9.8 | 33.8 | 47 | 4 | US-09-422-978-2958 | Sequence 2958, Ap  |
| 413 | 9.8 | 33.8 | 27 | 2 | US-08-457-733-12     | Sequence 12, Appli | C 486 | 9.8 | 33.8 | 47 | 4 | US-09-422-978-2979 | Sequence 2979, Ap  |
| 414 | 9.8 | 33.8 | 27 | 2 | US-08-457-986A-12    | Sequence 12, Appli | C 487 | 9.8 | 33.8 | 47 | 4 | US-09-422-978-3012 | Sequence 3012, Ap  |
| 415 | 9.8 | 33.8 | 27 | 5 | PCT-US93-01559-5     | Sequence 5, Appli  | C 488 | 9.8 | 33.8 | 47 | 4 | US-09-422-978-3201 | Sequence 3201, Ap  |
| 416 | 9.8 | 33.8 | 28 | 2 | US-08-859-998-1098   | Sequence 1098, Ap  | C 489 | 9.8 | 33.8 | 47 | 4 | US-09-422-978-3368 | Sequence 3368, Ap  |
| 417 | 9.8 | 33.8 | 28 | 3 | US-08-828-533-29     | Sequence 29, Appli | C 490 | 9.8 | 33.8 | 47 | 4 | US-09-422-978-3630 | Sequence 3630, Ap  |
| 418 | 9.8 | 33.8 | 28 | 3 | US-08-859-998-1114   | Sequence 1114, Ap  | C 491 | 9.8 | 33.8 | 47 | 5 | PCT-US93-12388-121 | Sequence 121, App  |
| 419 | 9.8 | 33.8 | 28 | 4 | US-09-225-928-1098   | Sequence 1098, Ap  | C 492 | 9.8 | 33.8 | 50 | 3 | US-08-833-167-84   | Sequence 84, Appl  |
| 420 | 9.8 | 33.8 | 28 | 4 | US-09-225-928-1114   | Sequence 1114, Ap  | C 493 | 9.8 | 33.8 | 50 | 3 | US-09-390-867A-31  | Sequence 31, Appl  |
| 421 | 9.8 | 33.8 | 28 | 4 | US-09-225-201B-1098  | Sequence 1098, Ap  | C 494 | 9.8 | 33.8 | 50 | 4 | US-09-548-260-31   | Sequence 31, Appl  |
| 422 | 9.8 | 33.8 | 28 | 4 | US-09-225-201B-1114  | Sequence 1114, Ap  | C 495 | 9.8 | 33.8 | 50 | 4 | US-09-344-837A-84  | Sequence 84, Appl  |
| 423 | 9.8 | 33.8 | 28 | 4 | US-09-772-156-29     | Sequence 29, Appli | C 496 | 9.8 | 33.8 | 50 | 4 | US-09-554-929-182  | Sequence 182, Appl |
| 424 | 9.8 | 33.8 | 29 | 1 | US-08-445-746-10     | Sequence 10, Appli | C 497 | 9.8 | 33.8 | 54 | 3 | US-08-369-822C-30  | Sequence 30, Appl  |
| 425 | 9.8 | 33.8 | 29 | 3 | US-09-008-722-10     | Sequence 10, Appli | C 498 | 9.8 | 33.8 | 54 | 3 | US-08-582-776C-45  | Sequence 45, Appl  |
| 426 | 9.8 | 33.8 | 30 | 1 | US-07-940-605A-13    | Sequence 13, Appli | C 499 | 9.8 | 33.8 | 54 | 3 | US-08-434-831B-42  | Sequence 42, Appl  |
| 427 | 9.8 | 33.8 | 30 | 1 | US-08-104-072B-13    | Sequence 13, Appli | C 500 | 9.8 | 33.8 | 55 | 3 | US-08-434-099A-17  | Sequence 17, Appli |
| 428 | 9.8 | 33.8 | 30 | 1 | US-08-182-530-4      | Sequence 4, Appli  | C 501 | 9.8 | 33.8 | 55 | 4 | US-09-509-748-4    | Sequence 4, Appli  |
| 429 | 9.8 | 33.8 | 30 | 1 | US-08-050-058B-4     | Sequence 4, Appli  | C 502 | 9.8 | 33.8 | 60 | 1 | US-08-464-531-18   | Sequence 18, Appl  |
| 430 | 9.8 | 33.8 | 30 | 1 | US-08-463-587A-4     | Sequence 4, Appli  | C 503 | 9.8 | 33.8 | 60 | 2 | US-08-461-598-18   | Sequence 18, Appl  |
| 431 | 9.8 | 33.8 | 30 | 2 | US-08-463-667A-7     | Sequence 7, Appli  | C 504 | 9.8 | 33.8 | 60 | 3 | US-08-322-137-18   | Sequence 18, Appl  |
| 432 | 9.8 | 33.8 | 30 | 2 | US-08-441-871-8      | Sequence 8, Appli  | C 505 | 9.8 | 33.8 | 60 | 3 | US-08-582-333A-9   | Sequence 9, Appli  |
| 433 | 9.8 | 33.8 | 30 | 2 | US-08-418-085-21     | Sequence 21, Appli | C 506 | 9.8 | 33.8 | 61 | 4 | US-09-313-221A-80  | Sequence 80, Appli |
| 434 | 9.8 | 33.8 | 30 | 2 | US-08-690-096-13     | Sequence 13, Appli | C 507 | 9.8 | 33.8 | 62 | 2 | US-08-210-763B-5   | Sequence 5, Appli  |
| 435 | 9.8 | 33.8 | 30 | 3 | US-08-923-854-4      | Sequence 4, Appli  | C 508 | 9.8 | 33.8 | 62 | 4 | US-09-106-075A-5   | Sequence 5, Appli  |
| 436 | 9.8 | 33.8 | 30 | 3 | US-09-099-011A-21    | Sequence 21, Appli | C 509 | 9.8 | 33.8 | 63 | 2 | US-09-159-385-7    | Sequence 7, Appli  |
| 437 | 9.8 | 33.8 | 30 | 4 | US-09-490-825-2      | Sequence 2, Appli  | C 510 | 9.8 | 33.8 | 63 | 3 | US-09-186-277-7    | Sequence 7, Appli  |
| 438 | 9.8 | 33.8 | 30 | 4 | US-09-898-627-2      | Sequence 2, Appli  | C 511 | 9.8 | 33.8 | 64 | 1 | US-08-471-364A-2   | Sequence 2, Appli  |
| 439 | 9.8 | 33.8 | 30 | 4 | US-09-397-955C-16    | Sequence 16, Appli | C 512 | 9.8 | 33.8 | 67 | 3 | US-08-483-511-55   | Sequence 55, Appli |
| 440 | 9.8 | 33.8 | 30 | 4 | US-09-098-877B-21    | Sequence 21, Appli | C 513 | 9.8 | 33.8 | 67 | 5 | PCT-US93-01009-55  | Sequence 55, Appli |
| 441 | 9.8 | 33.8 | 30 | 4 | US-09-381-393A-7     | Sequence 7, Appli  | C 514 | 9.8 | 33.8 | 68 | 2 | US-09-121-527-3    | Sequence 3, Appli  |
| 442 | 9.8 | 33.8 | 30 | 5 | PCT-US91-09133-4     | Sequence 4, Appli  | C 515 | 9.8 | 33.8 | 70 | 1 | US-08-434-001-179  | Sequence 179, App  |
| 443 | 9.8 | 33.8 | 31 | 4 | US-09-206-898-22     | Sequence 22, Appli | C 516 | 9.8 | 33.8 | 70 | 1 | US-08-433-585-179  | Sequence 179, App  |
| 444 | 9.8 | 33.8 | 31 | 4 | US-08-201-118-15     | Sequence 15, Appli | C 517 | 9.8 | 33.8 | 70 | 1 | US-08-434-425-179  | Sequence 179, App  |
| 445 | 9.8 | 33.8 | 33 | 1 | US-08-201-118-21     | Sequence 21, Appli | C 518 | 9.8 | 33.8 | 70 | 2 | US-08-437-667-179  | Sequence 179, App  |
| 446 | 9.8 | 33.8 | 33 | 2 | US-08-238-821B-15    | Sequence 15, Appli | C 519 | 9.8 | 33.8 | 70 | 3 | US-08-906-955-179  | Sequence 179, App  |
| 447 | 9.8 | 33.8 | 33 | 2 | US-08-238-821B-21    | Sequence 21, Appli | C 520 | 9.8 | 33.8 | 70 | 3 | US-08-945-909-179  | Sequence 179, App  |
| 448 | 9.8 | 33.8 | 33 | 3 | US-09-855-341-13     | Sequence 13, Appli | C 521 | 9.8 | 33.8 | 70 | 4 | US-09-396-002A-179 | Sequence 179, App  |
| 449 | 9.8 | 33.8 | 33 | 5 | PCT-US95-05744-15    | Sequence 15, Appli | C 522 | 9.8 | 33.8 | 70 | 4 | US-10-077-319-179  | Sequence 179, App  |
| 450 | 9.8 | 33.8 | 33 | 5 | PCT-US95-05744-21    | Sequence 21, Appli | C 523 | 9.8 | 33.8 | 70 | 5 | PCT-US96-06060-179 | Sequence 179, App  |
| 451 | 9.8 | 33.8 | 34 | 1 | US-07-982-174-4      | Sequence 4, Appli  | C 524 | 9.8 | 33.8 | 71 | 2 | US-08-482-182-45   | Sequence 45, Appl  |
| 452 | 9.8 | 33.8 | 34 | 1 | US-08-589-528-4      | Sequence 4, Appli  | C 525 | 9.8 | 33.8 | 71 | 2 | US-08-482-182-45   | Sequence 45, Appl  |
| 453 | 9.8 | 33.8 | 34 | 2 | US-08-392-625-7      | Sequence 7, Appli  | C 526 | 9.8 | 33.8 | 77 | 4 | US-09-621-976-8652 | Sequence 8652, Ap  |
| 454 | 9.8 | 33.8 | 34 | 2 | US-08-466-961A-7     | Sequence 7, Appli  | C 527 | 9.8 | 33.8 | 78 | 1 | US-08-817-335-2    | Sequence 2, Appli  |
| 455 | 9.8 | 33.8 | 34 | 3 | US-07-901-713A-19    | Sequence 19, Appli | C 528 | 9.8 | 33.8 | 78 | 3 | US-08-817-335-2    | Sequence 2, Appli  |
| 456 | 9.8 | 33.8 | 34 | 5 | PCT-US93-11492-4     | Sequence 4, Appli  | C 529 | 9.8 | 33.8 | 78 | 4 | US-09-397-680A-1   | Sequence 1, Appli  |
| 457 | 9.8 | 33.8 | 35 | 4 | US-09-381-393A-3     | Sequence 3, Appli  | C 530 | 9.8 | 33.8 | 78 | 4 | US-09-949-404-1    | Sequence 40, Appli |
| 458 | 9.8 | 33.8 | 36 | 4 | US-09-198-115C-19    | Sequence 19, Appli | C 531 | 9.8 | 33.8 | 78 | 5 | PCT-US96-09448-40  | Sequence 40, Appli |
| 459 | 9.8 | 33.8 | 37 | 1 | US-08-464-531-4      | Sequence 4, Appli  | C 532 | 9.8 | 33.8 | 80 | 1 | US-07-832-905B-61  | Sequence 61, Appli |
| 460 | 9.8 | 33.8 | 37 | 1 | US-08-461-598-4      | Sequence 4, Appli  | C 533 | 9.8 | 33.8 | 80 | 1 | US-07-832-905B-62  | Sequence 62, Appli |
| 461 | 9.8 | 33.8 | 37 | 3 | US-08-322-137-4      | Sequence 4, Appli  | C 534 | 9.8 | 33.8 | 80 | 2 | US-08-700-757-61   | Sequence 61, Appli |
| 462 | 9.8 | 33.8 | 40 | 3 | US-08-833-167-85     | Sequence 85, Appli | C 535 | 9.8 | 33.8 | 80 | 2 | US-08-700-757-61   | Sequence 61, Appli |
| 463 | 9.8 | 33.8 | 40 | 3 | US-09-344-837A-85    | Sequence 85, Appli | C 536 | 9.8 | 33.1 | 22 | 4 | US-09-026-033-5    | Sequence 5, Appli  |
| 464 | 9.8 | 33.8 | 42 | 3 | US-08-434-099A-16    | Sequence 16, Appli | C 537 | 9.8 | 33.1 | 24 | 2 | US-08-451-822A-11  | Sequence 11, Appli |
| 465 | 9.8 | 33.8 | 43 | 3 | US-09-150-805-5      | Sequence 5, Appli  | C 538 | 9.8 | 33.1 | 24 | 4 | US-08-323-430-11   | Sequence 11, Appli |



|       |     |      |    |   |                     |                    |     |     |      |    |   |                      |                    |
|-------|-----|------|----|---|---------------------|--------------------|-----|-----|------|----|---|----------------------|--------------------|
| C 685 | 9.6 | 33.1 | 60 | 4 | US-09-496-398-32    | Sequence 32, Appl  | 758 | 9.4 | 32.4 | 22 | 1 | US-08-379-078-297    | Sequence 297, App  |
| C 686 | 9.6 | 33.1 | 60 | 4 | US-09-722-825-57    | Sequence 57, Appl  | 759 | 9.4 | 32.4 | 22 | 1 | US-08-379-078-298    | Sequence 298, App  |
| C 687 | 9.6 | 33.1 | 60 | 4 | US-09-722-487-57    | Sequence 57, Appl  | 760 | 9.4 | 32.4 | 22 | 1 | US-08-743-637B-239   | Sequence 239, App  |
| C 688 | 9.6 | 33.1 | 60 | 4 | US-09-722-708-57    | Sequence 57, Appl  | 761 | 9.4 | 32.4 | 22 | 3 | US-08-876-885-19     | Sequence 19, Appl  |
| C 689 | 9.6 | 33.1 | 60 | 4 | US-08-956-171E-2347 | Sequence 2347, Ap  | 762 | 9.4 | 32.4 | 22 | 4 | US-09-445-283C-45    | Sequence 45, Appl  |
| C 690 | 9.6 | 33.1 | 61 | 1 | US-07-744-282C-106  | Sequence 106, App  | 763 | 9.4 | 32.4 | 22 | 3 | US-08-864-377E-16    | Sequence 16, Appl  |
| C 691 | 9.6 | 33.1 | 61 | 5 | PCT-US92-06821A-57  | Sequence 52, Appl  | 764 | 9.4 | 32.4 | 24 | 3 | US-08-508-778A-6     | Sequence 6, Appl   |
| C 692 | 9.6 | 33.1 | 63 | 3 | US-07-921-104D-32   | Sequence 37, Appl  | 765 | 9.4 | 32.4 | 24 | 3 | US-08-641-291A-50    | Sequence 50, Appl  |
| C 693 | 9.6 | 33.1 | 63 | 6 | 5474935-2           | Sequence 37, Appl  | 766 | 9.4 | 32.4 | 24 | 3 | US-09-327-223-25     | Sequence 25, Appl  |
| C 694 | 9.6 | 33.1 | 63 | 6 | 5474935-2           | Patent No. 5474935 | 767 | 9.4 | 32.4 | 24 | 4 | US-09-302-681-45     | Sequence 45, Appl  |
| C 695 | 9.6 | 33.1 | 65 | 1 | US-08-391-339-28    | Sequence 28, Appl  | 768 | 9.4 | 32.4 | 24 | 5 | PCT-US95-12608-25    | Sequence 25, Appl  |
| C 696 | 9.6 | 33.1 | 65 | 1 | US-08-484-274A-28   | Sequence 28, Appl  | 769 | 9.4 | 32.4 | 25 | 1 | US-07-771-022F-7     | Sequence 7, Appl   |
| C 697 | 9.6 | 33.1 | 65 | 2 | US-08-188-583-40    | Sequence 40, Appl  | 770 | 9.4 | 32.4 | 25 | 4 | US-09-866-108A-11545 | Sequence 11545, A  |
| C 698 | 9.6 | 33.1 | 66 | 3 | US-08-956-171E-1641 | Sequence 1641, Ap  | 771 | 9.4 | 32.4 | 25 | 4 | US-09-866-108A-11546 | Sequence 11546, A  |
| C 699 | 9.6 | 33.1 | 68 | 3 | US-09-242-650A-54   | Sequence 54, Appl  | 772 | 9.4 | 32.4 | 25 | 4 | US-09-866-108A-11547 | Sequence 11547, A  |
| C 700 | 9.6 | 33.1 | 69 | 4 | US-09-908-855-54    | Sequence 54, Appl  | 773 | 9.4 | 32.4 | 25 | 4 | US-09-866-108A-11548 | Sequence 11548, A  |
| C 701 | 9.6 | 33.1 | 69 | 4 | US-09-134-360C-20   | Sequence 20, Appl  | 774 | 9.4 | 32.4 | 25 | 4 | US-09-866-108A-11549 | Sequence 11549, A  |
| C 702 | 9.6 | 33.1 | 71 | 2 | US-08-477-527A-22   | Sequence 22, Appl  | 775 | 9.4 | 32.4 | 25 | 4 | US-09-866-108A-11550 | Sequence 11550, A  |
| C 703 | 9.6 | 33.1 | 71 | 3 | US-08-481-710-22    | Sequence 22, Appl  | 776 | 9.4 | 32.4 | 25 | 4 | US-09-866-108A-11551 | Sequence 11551, A  |
| C 704 | 9.6 | 33.1 | 71 | 3 | US-09-275-850-143   | Sequence 143, App  | 777 | 9.4 | 32.4 | 25 | 4 | US-09-866-108A-11552 | Sequence 11552, A  |
| C 705 | 9.6 | 33.1 | 71 | 3 | US-09-363-939A-67   | Sequence 67, Appl  | 778 | 9.4 | 32.4 | 25 | 4 | US-09-866-108A-11553 | Sequence 11553, A  |
| C 706 | 9.6 | 33.1 | 71 | 5 | PCT-US96-09537-22   | Sequence 22, Appl  | 779 | 9.4 | 32.4 | 25 | 4 | US-09-866-108A-11554 | Sequence 11554, A  |
| C 707 | 9.6 | 33.1 | 74 | 4 | US-09-837-644-7     | Sequence 71, Appl  | 780 | 9.4 | 32.4 | 25 | 4 | US-09-866-108A-11555 | Sequence 11555, A  |
| C 708 | 9.6 | 33.1 | 78 | 1 | US-08-477-877B-61   | Sequence 61, Appl  | 781 | 9.4 | 32.4 | 26 | 1 | US-07-828-798C-3     | Sequence 3, Appl   |
| C 709 | 9.6 | 33.1 | 78 | 1 | US-08-477-877B-63   | Sequence 63, Appl  | 782 | 9.4 | 32.4 | 26 | 1 | US-08-514-921-33     | Sequence 33, Appl  |
| C 710 | 9.6 | 33.1 | 78 | 1 | US-08-472-281A-61   | Sequence 61, Appl  | 783 | 9.4 | 32.4 | 26 | 2 | US-08-315-868A-3     | Sequence 3, Appl   |
| C 711 | 9.6 | 33.1 | 78 | 1 | US-08-472-281A-63   | Sequence 63, Appl  | 784 | 9.4 | 32.4 | 26 | 3 | US-08-495-819B-3     | Sequence 3, Appl   |
| C 712 | 9.6 | 33.1 | 78 | 2 | US-08-477-989B-61   | Sequence 61, Appl  | 785 | 9.4 | 32.4 | 26 | 3 | US-08-478-316-71     | Sequence 71, Appl  |
| C 713 | 9.6 | 33.1 | 78 | 2 | US-08-477-989B-63   | Sequence 63, Appl  | 786 | 9.4 | 32.4 | 26 | 3 | US-08-478-316-72     | Sequence 72, Appl  |
| C 714 | 9.4 | 32.4 | 15 | 1 | US-08-182-968A-270  | Sequence 270, App  | 787 | 9.4 | 32.4 | 26 | 3 | US-09-245-041-46     | Sequence 46, Appl  |
| C 715 | 9.4 | 32.4 | 15 | 1 | US-08-182-968A-271  | Sequence 271, App  | 788 | 9.4 | 32.4 | 26 | 4 | US-09-019-793A-71    | Sequence 71, Appl  |
| C 716 | 9.4 | 32.4 | 15 | 1 | US-08-291-932A-237  | Sequence 237, App  | 789 | 9.4 | 32.4 | 26 | 4 | US-09-019-793A-72    | Sequence 72, Appl  |
| C 717 | 9.4 | 32.4 | 15 | 1 | US-08-291-932A-238  | Sequence 238, App  | 790 | 9.4 | 32.4 | 26 | 4 | US-09-019-793A-72    | Sequence 72, Appl  |
| C 718 | 9.4 | 32.4 | 15 | 2 | US-08-821-355A-4    | Sequence 4, Appl   | 791 | 9.4 | 32.4 | 26 | 4 | US-09-013-3          | Sequence 3, Appl   |
| C 719 | 9.4 | 32.4 | 15 | 2 | US-08-774-306A-270  | Sequence 270, App  | 792 | 9.4 | 32.4 | 27 | 2 | US-08-859-998-1350   | Sequence 1350, Ap  |
| C 720 | 9.4 | 32.4 | 15 | 2 | US-08-774-306A-271  | Sequence 271, App  | 793 | 9.4 | 32.4 | 27 | 2 | US-09-225-928-1350   | Sequence 1350, Ap  |
| C 721 | 9.4 | 32.4 | 15 | 2 | US-09-003-687A-4    | Sequence 4, Appl   | 794 | 9.4 | 32.4 | 28 | 3 | US-09-225-928-1350   | Sequence 1350, Ap  |
| C 722 | 9.4 | 32.4 | 15 | 3 | US-09-064-156A-270  | Sequence 270, App  | 795 | 9.4 | 32.4 | 28 | 3 | US-08-893-440-34     | Sequence 34, Appl  |
| C 723 | 9.4 | 32.4 | 15 | 3 | US-09-064-156A-271  | Sequence 271, App  | 796 | 9.4 | 32.4 | 28 | 4 | US-09-367-895-36     | Sequence 36, Appl  |
| C 724 | 9.4 | 32.4 | 15 | 3 | US-09-136-605-4     | Sequence 4, Appl   | 797 | 9.4 | 32.4 | 29 | 4 | US-09-396-154-58     | Sequence 58, Appl  |
| C 725 | 9.4 | 32.4 | 16 | 3 | US-09-136-605-13    | Sequence 13, Appl  | 798 | 9.4 | 32.4 | 29 | 4 | US-08-184-009-201    | Sequence 201, App  |
| C 726 | 9.4 | 32.4 | 16 | 4 | US-09-479-005A-302  | Sequence 302, App  | 799 | 9.4 | 32.4 | 30 | 2 | US-08-458-356-201    | Sequence 201, App  |
| C 727 | 9.4 | 32.4 | 17 | 1 | US-08-373-124A-756  | Sequence 756, App  | 800 | 9.4 | 32.4 | 30 | 2 | US-08-458-356-201    | Sequence 201, App  |
| C 728 | 9.4 | 32.4 | 17 | 1 | US-08-373-124A-1825 | Sequence 1825, Ap  | 801 | 9.4 | 32.4 | 30 | 2 | US-08-458-356-201    | Sequence 201, App  |
| C 729 | 9.4 | 32.4 | 17 | 1 | US-08-435-628-756   | Sequence 756, App  | 802 | 9.4 | 32.4 | 30 | 3 | US-08-458-356-201    | Sequence 201, App  |
| C 730 | 9.4 | 32.4 | 17 | 1 | US-08-435-628-1825  | Sequence 1825, Ap  | 803 | 9.4 | 32.4 | 30 | 3 | US-08-458-356-201    | Sequence 201, App  |
| C 731 | 9.4 | 32.4 | 17 | 4 | US-09-371-772B-5130 | Sequence 5130, Ap  | 804 | 9.4 | 32.4 | 30 | 3 | US-08-460-736-201    | Sequence 201, App  |
| C 732 | 9.4 | 32.4 | 17 | 4 | US-09-371-772B-5131 | Sequence 5131, Ap  | 805 | 9.4 | 32.4 | 30 | 4 | US-09-535-370-201    | Sequence 370, Appl |
| C 733 | 9.4 | 32.4 | 17 | 4 | US-09-371-772B-5132 | Sequence 5132, Ap  | 806 | 9.4 | 32.4 | 31 | 1 | US-08-390-850-84     | Sequence 84, Appl  |
| C 734 | 9.4 | 32.4 | 17 | 4 | US-09-371-772B-5133 | Sequence 5133, Ap  | 807 | 9.4 | 32.4 | 31 | 1 | US-08-390-850-85     | Sequence 85, Appl  |
| C 735 | 9.4 | 32.4 | 17 | 4 | US-09-866-108A-6653 | Sequence 6653, Ap  | 808 | 9.4 | 32.4 | 31 | 1 | US-08-390-850-86     | Sequence 86, Appl  |
| C 736 | 9.4 | 32.4 | 17 | 4 | US-09-866-108A-6654 | Sequence 6654, Ap  | 809 | 9.4 | 32.4 | 31 | 1 | US-08-390-850-87     | Sequence 87, Appl  |
| C 737 | 9.4 | 32.4 | 17 | 4 | US-09-866-108A-6655 | Sequence 6655, Ap  | 810 | 9.4 | 32.4 | 31 | 1 | US-08-435-634-84     | Sequence 84, Appl  |
| C 738 | 9.4 | 32.4 | 18 | 2 | US-09-200-141-37    | Sequence 37, Appl  | 811 | 9.4 | 32.4 | 31 | 1 | US-08-435-634-85     | Sequence 85, Appl  |
| C 739 | 9.4 | 32.4 | 18 | 4 | US-09-422-978-4252  | Sequence 4252, Ap  | 812 | 9.4 | 32.4 | 31 | 1 | US-08-435-634-86     | Sequence 86, Appl  |
| C 740 | 9.4 | 32.4 | 18 | 5 | PCT-US94-06331A-53  | Sequence 53, Appl  | 813 | 9.4 | 32.4 | 31 | 1 | US-09-292-225-26     | Sequence 26, Appl  |
| C 741 | 9.4 | 32.4 | 19 | 4 | US-09-422-978-4227  | Sequence 4227, Ap  | 814 | 9.4 | 32.4 | 31 | 3 | US-09-292-225-26     | Sequence 26, Appl  |
| C 742 | 9.4 | 32.4 | 19 | 4 | US-09-422-978-4227  | Sequence 4227, Ap  | 815 | 9.4 | 32.4 | 32 | 3 | US-09-292-225-26     | Sequence 26, Appl  |
| C 743 | 9.4 | 32.4 | 20 | 1 | US-08-222-177A-319  | Sequence 319, App  | 816 | 9.4 | 32.4 | 32 | 4 | US-08-753-750B-22    | Sequence 22, Appl  |
| C 744 | 9.4 | 32.4 | 20 | 1 | US-08-564-002-11    | Sequence 11, Appl  | 817 | 9.4 | 32.4 | 32 | 4 | US-08-753-750B-25    | Sequence 25, Appl  |
| C 745 | 9.4 | 32.4 | 20 | 3 | US-09-009-913-329   | Sequence 329, App  | 818 | 9.4 | 32.4 | 33 | 1 | US-08-073-807A-13    | Sequence 13, Appl  |
| C 746 | 9.4 | 32.4 | 20 | 3 | US-09-311-260-58    | Sequence 58, Appl  | 819 | 9.4 | 32.4 | 33 | 1 | US-08-450-944-11     | Sequence 11, Appl  |
| C 747 | 9.4 | 32.4 | 20 | 4 | US-09-629-645A-47   | Sequence 47, Appl  | 820 | 9.4 | 32.4 | 33 | 5 | PCT-US96-07709-11    | Sequence 11, Appl  |
| C 748 | 9.4 | 32.4 | 20 | 4 | US-09-861-753-42    | Sequence 42, Appl  | 821 | 9.4 | 32.4 | 33 | 5 | PCT-US96-07709-11    | Sequence 11, Appl  |
| C 749 | 9.4 | 32.4 | 20 | 4 | US-09-222-938A-98   | Sequence 98, Appl  | 822 | 9.4 | 32.4 | 34 | 1 | US-08-309-604-6      | Sequence 6, Appl   |
| C 750 | 9.4 | 32.4 | 20 | 4 | US-09-517-467B-185  | Sequence 185, App  | 823 | 9.4 | 32.4 | 34 | 3 | US-09-075-019-12     | Sequence 12, Appl  |
| C 751 | 9.4 | 32.4 | 20 | 4 | US-09-422-978-9295  | Sequence 9295, Ap  | 824 | 9.4 | 32.4 | 34 | 3 | US-09-235-028-81     | Sequence 81, Appl  |
| C 752 | 9.4 | 32.4 | 20 | 4 | US-10-009-457-14    | Sequence 14, Appl  | 825 | 9.4 | 32.4 | 34 | 3 | US-09-693-542-84     | Sequence 84, Appl  |
| C 753 | 9.4 | 32.4 | 21 | 4 | US-09-422-978-7010  | Sequence 7010, Ap  | 826 | 9.4 | 32.4 | 35 | 4 | US-09-495-052-43     | Sequence 43, Appl  |
| C 754 | 9.4 | 32.4 | 21 | 4 | US-09-422-978-9499  | Sequence 9499, Ap  | 827 | 9.4 | 32.4 | 35 | 4 | US-09-463-125D-11    | Sequence 11, Appl  |
| C 755 | 9.4 | 32.4 | 21 | 4 | US-09-422-978-10994 | Sequence 10994, A  | 828 | 9.4 | 32.4 | 36 | 1 | US-08-363-240A-426   | Sequence 426, App  |
| C 756 | 9.4 | 32.4 | 22 | 1 | US-08-379-081B-237  | Sequence 237, App  | 829 | 9.4 | 32.4 | 38 | 1 | US-09-474-432B-1249  | Sequence 1249, App |
| C 757 | 9.4 | 32.4 | 22 | 1 | US-08-379-081B-238  | Sequence 238, App  | 830 | 9.4 | 32.4 | 38 | 4 | US-09-476-387-1248   | Sequence 1248, Ap  |

|       |     |      |    |   |                     |                   |       |     |      |    |   |                     |                    |
|-------|-----|------|----|---|---------------------|-------------------|-------|-----|------|----|---|---------------------|--------------------|
| 831   | 9.4 | 32.4 | 39 | 4 | US-09-622-540A-17   | Sequence 17, Appl | C 904 | 9.4 | 32.4 | 61 | 4 | US-08-638-524B-21   | Sequence 21, Appl  |
| 832   | 9.4 | 32.4 | 39 | 4 | US-09-622-540A-17   | Sequence 17, Appl | 905   | 9.4 | 32.4 | 62 | 4 | US-09-502-558-20    | Sequence 20, Appl  |
| C 833 | 9.4 | 32.4 | 39 | 4 | US-09-350-982C-10   | Sequence 10, Appl | 906   | 9.4 | 32.4 | 62 | 4 | US-08-956-171E-1684 | Sequence 1684, Ap  |
| C 834 | 9.4 | 32.4 | 40 | 2 | US-08-628-422-48    | Sequence 48, Appl | 907   | 9.4 | 32.4 | 63 | 2 | US-08-350-260A-201  | Sequence 201, App  |
| C 835 | 9.4 | 32.4 | 40 | 2 | US-09-223-139-7     | Sequence 7, Appl  | 908   | 9.4 | 32.4 | 63 | 4 | US-09-104-337A-201  | Sequence 201, App  |
| C 836 | 9.4 | 32.4 | 40 | 4 | US-09-426-082B-418  | Sequence 7, Appl  | 909   | 9.4 | 32.4 | 64 | 4 | US-09-586-546-40    | Sequence 40, Appl  |
| C 837 | 9.4 | 32.4 | 41 | 3 | US-08-813-507-152   | Sequence 152, App | C 910 | 9.4 | 32.4 | 64 | 4 | US-09-065-918B-4    | Sequence 4, Appl   |
| C 838 | 9.4 | 32.4 | 41 | 4 | US-08-464-453-152   | Sequence 152, App | 911   | 9.4 | 32.4 | 71 | 2 | US-08-894-578-130   | Sequence 190, App  |
| C 839 | 9.4 | 32.4 | 41 | 4 | US-09-350-982C-8    | Sequence 8, Appl  | 912   | 9.4 | 32.4 | 71 | 4 | US-09-364-902-43    | Sequence 43, Appl  |
| C 840 | 9.4 | 32.4 | 41 | 4 | US-09-442-021-23    | Sequence 23, Appl | 913   | 9.4 | 32.4 | 71 | 4 | US-09-363-939A-28   | Sequence 28, Appl  |
| C 841 | 9.4 | 32.4 | 42 | 3 | US-09-237-712-30    | Sequence 30, Appl | 914   | 9.4 | 32.4 | 71 | 4 | US-09-854-662-43    | Sequence 43, Appl  |
| C 842 | 9.4 | 32.4 | 43 | 3 | US-09-237-712-30    | Sequence 30, Appl | 915   | 9.4 | 32.4 | 72 | 3 | US-08-821-827C-28   | Sequence 28, Appl  |
| C 843 | 9.4 | 32.4 | 45 | 3 | US-09-312-285-6     | Sequence 6, Appl  | C 916 | 9.4 | 32.4 | 72 | 4 | US-09-290-202B-28   | Sequence 28, Appl  |
| C 844 | 9.4 | 32.4 | 45 | 3 | US-09-312-285-6     | Sequence 6, Appl  | 917   | 9.4 | 32.4 | 72 | 4 | US-09-313-294A-4205 | Sequence 4205, Ap  |
| C 845 | 9.4 | 32.4 | 45 | 3 | US-09-312-286-6     | Sequence 6, Appl  | 918   | 9.4 | 32.4 | 78 | 4 | US-09-621-976-12398 | Sequence 12398, A  |
| C 846 | 9.4 | 32.4 | 45 | 3 | US-09-312-286-6     | Sequence 6, Appl  | 919   | 9.4 | 32.4 | 79 | 1 | US-08-471-985A-56   | Sequence 56, Appl  |
| C 847 | 9.4 | 32.4 | 45 | 3 | US-09-312-038-6     | Sequence 6, Appl  | C 920 | 9.4 | 32.4 | 79 | 5 | PCT-US95-12401A-56  | Sequence 56, Appl  |
| C 848 | 9.4 | 32.4 | 45 | 3 | US-09-312-038-6     | Sequence 6, Appl  | 921   | 9.4 | 32.4 | 80 | 1 | US-08-471-985A-53   | Sequence 53, Appl  |
| C 849 | 9.4 | 32.4 | 45 | 3 | US-09-728-764-6     | Sequence 6, Appl  | C 922 | 9.4 | 32.4 | 80 | 1 | US-08-471-985A-71   | Sequence 71, Appl  |
| C 850 | 9.4 | 32.4 | 45 | 4 | US-09-728-764-6     | Sequence 6, Appl  | C 923 | 9.4 | 32.4 | 80 | 1 | US-08-471-985A-78   | Sequence 78, Appl  |
| C 851 | 9.4 | 32.4 | 45 | 4 | US-09-312-304B-4    | Sequence 4, Appl  | C 924 | 9.4 | 32.4 | 80 | 1 | US-08-472-258A-157  | Sequence 157, App  |
| C 852 | 9.4 | 32.4 | 45 | 4 | US-09-312-304B-5    | Sequence 5, Appl  | C 925 | 9.4 | 32.4 | 80 | 1 | US-08-472-258B-157  | Sequence 157, App  |
| C 853 | 9.4 | 32.4 | 45 | 4 | US-09-728-792-6     | Sequence 6, Appl  | C 926 | 9.4 | 32.4 | 80 | 3 | US-08-472-256B-157  | Sequence 157, App  |
| C 854 | 9.4 | 32.4 | 45 | 4 | US-09-728-792-7     | Sequence 7, Appl  | C 927 | 9.4 | 32.4 | 80 | 3 | US-08-952-793-157   | Sequence 157, App  |
| C 855 | 9.4 | 32.4 | 45 | 4 | US-09-850-964-6     | Sequence 6, Appl  | C 928 | 9.4 | 32.4 | 80 | 3 | US-08-952-793-157   | Sequence 157, App  |
| C 856 | 9.4 | 32.4 | 45 | 4 | US-09-850-964-7     | Sequence 7, Appl  | C 929 | 9.4 | 32.4 | 80 | 4 | US-09-849-928-157   | Sequence 157, App  |
| C 857 | 9.4 | 32.4 | 47 | 4 | US-09-641-638-1106  | Sequence 1106, Ap | C 930 | 9.4 | 32.4 | 80 | 4 | US-09-849-928-157   | Sequence 157, App  |
| C 858 | 9.4 | 32.4 | 47 | 4 | US-09-422-978-952   | Sequence 952, App | C 931 | 9.4 | 32.4 | 80 | 5 | PCT-US95-12401A-53  | Sequence 53, Appl  |
| C 859 | 9.4 | 32.4 | 47 | 4 | US-09-422-978-952   | Sequence 952, App | C 932 | 9.4 | 32.4 | 80 | 5 | PCT-US95-12401A-71  | Sequence 71, Appl  |
| C 860 | 9.4 | 32.4 | 47 | 4 | US-09-422-978-1054  | Sequence 1054, Ap | C 933 | 9.4 | 32.4 | 80 | 5 | PCT-US95-12401A-78  | Sequence 78, Appl  |
| C 861 | 9.4 | 32.4 | 47 | 4 | US-09-422-978-1681  | Sequence 1681, Ap | C 934 | 9.4 | 32.4 | 80 | 5 | PCT-US96-09455A-157 | Sequence 157, App  |
| C 862 | 9.4 | 32.4 | 47 | 4 | US-09-422-978-1965  | Sequence 1965, Ap | C 935 | 9.4 | 32.4 | 80 | 5 | PCT-US96-09455A-172 | Sequence 172, App  |
| C 863 | 9.4 | 32.4 | 47 | 4 | US-09-432-978-2318  | Sequence 2318, Ap | C 936 | 9.4 | 32.4 | 17 | 4 | US-09-827-998-846   | Sequence 846, App  |
| C 864 | 9.4 | 32.4 | 47 | 4 | US-09-432-978-2337  | Sequence 2337, Ap | C 937 | 9.4 | 32.4 | 18 | 1 | US-08-599-253-22    | Sequence 22, Appl  |
| C 865 | 9.4 | 32.4 | 47 | 4 | US-09-432-978-3699  | Sequence 3699, Ap | C 938 | 9.4 | 32.4 | 18 | 1 | US-08-436-074-22    | Sequence 22, Appl  |
| C 866 | 9.4 | 32.4 | 47 | 4 | US-09-432-978-3710  | Sequence 3710, Ap | C 939 | 9.4 | 32.4 | 18 | 5 | PCT-US96-06352-22   | Sequence 22, Appl  |
| C 867 | 9.4 | 32.4 | 48 | 4 | US-09-586-546-43    | Sequence 43, Appl | C 940 | 9.4 | 32.4 | 18 | 5 | PCT-US96-06583-22   | Sequence 22, Appl  |
| C 868 | 9.4 | 32.4 | 48 | 4 | US-09-065-914B-2    | Sequence 2, Appl  | C 941 | 9.4 | 32.4 | 19 | 1 | US-08-379-081B-130  | Sequence 130, Appl |
| C 869 | 9.4 | 32.4 | 48 | 4 | US-09-623-326-37    | Sequence 37, Appl | C 942 | 9.4 | 32.4 | 19 | 1 | US-08-379-081B-146  | Sequence 146, App  |
| C 870 | 9.4 | 32.4 | 49 | 3 | US-09-109-063-28    | Sequence 28, Appl | C 943 | 9.4 | 32.4 | 19 | 1 | US-08-379-078-130   | Sequence 130, App  |
| C 871 | 9.4 | 32.4 | 49 | 3 | US-09-109-063-29    | Sequence 29, Appl | C 944 | 9.4 | 32.4 | 19 | 1 | US-08-379-078-130   | Sequence 130, App  |
| C 872 | 9.4 | 32.4 | 49 | 3 | US-08-874-825-46    | Sequence 46, Appl | C 945 | 9.4 | 32.4 | 19 | 3 | US-08-651-999A-8    | Sequence 8, Appl   |
| C 873 | 9.4 | 32.4 | 49 | 3 | US-08-663-824-46    | Sequence 46, Appl | C 946 | 9.4 | 32.4 | 19 | 3 | US-08-532-896-53    | Sequence 53, Appl  |
| C 874 | 9.4 | 32.4 | 49 | 4 | US-08-231-303-46    | Sequence 46, Appl | C 947 | 9.4 | 32.4 | 19 | 3 | US-08-561-810-84    | Sequence 84, Appl  |
| C 875 | 9.4 | 32.4 | 49 | 4 | US-09-448-310-28    | Sequence 28, Appl | C 948 | 9.4 | 32.4 | 19 | 3 | US-08-352-902D-84   | Sequence 84, Appl  |
| C 876 | 9.4 | 32.4 | 49 | 4 | US-09-448-310-29    | Sequence 29, Appl | C 949 | 9.4 | 32.4 | 19 | 3 | US-09-385-752-8     | Sequence 8, Appl   |
| C 877 | 9.4 | 32.4 | 50 | 3 | US-09-237-712-80    | Sequence 80, Appl | C 950 | 9.4 | 32.4 | 19 | 4 | US-09-343-681C-85   | Sequence 85, Appl  |
| C 878 | 9.4 | 32.4 | 50 | 4 | US-09-554-929-12    | Sequence 12, Appl | C 951 | 9.4 | 32.4 | 19 | 4 | US-09-375-318-29    | Sequence 29, Appl  |
| C 879 | 9.4 | 32.4 | 51 | 4 | US-08-956-171E-2665 | Sequence 2665, Ap | C 952 | 9.4 | 32.4 | 19 | 4 | US-09-375-318-43    | Sequence 43, Appl  |
| C 880 | 9.4 | 32.4 | 51 | 4 | US-08-956-171E-2477 | Sequence 2477, Ap | C 953 | 9.4 | 32.4 | 19 | 4 | US-09-265-503B-84   | Sequence 84, Appl  |
| C 881 | 9.4 | 32.4 | 51 | 4 | US-08-621-976-3693  | Sequence 693, Ap  | C 954 | 9.4 | 32.4 | 20 | 1 | US-08-190-711-4     | Sequence 4, Appl   |
| C 882 | 9.4 | 32.4 | 52 | 4 | US-08-443-199C-737  | Sequence 737, App | C 955 | 9.4 | 32.4 | 20 | 1 | US-08-455-896-12    | Sequence 12, Appl  |
| C 883 | 9.4 | 32.4 | 52 | 4 | US-08-956-171E-2653 | Sequence 91, Appl | C 956 | 9.4 | 32.4 | 20 | 2 | US-08-249-386A-1    | Sequence 1, Appl   |
| C 884 | 9.4 | 32.4 | 54 | 1 | US-07-744-282C-91   | Sequence 91, Appl | C 957 | 9.4 | 32.4 | 20 | 2 | US-08-933-149-12    | Sequence 12, Appl  |
| C 885 | 9.4 | 32.4 | 54 | 5 | PCT-US92-06821A-74  | Sequence 74, Appl | C 958 | 9.4 | 32.4 | 20 | 3 | US-09-082-253-12    | Sequence 12, Appl  |
| C 886 | 9.4 | 32.4 | 56 | 1 | US-08-102-474-10    | Sequence 10, Appl | C 959 | 9.4 | 32.4 | 20 | 3 | US-08-487-799-66    | Sequence 66, Appl  |
| C 887 | 9.4 | 32.4 | 56 | 1 | US-08-414-019A-10   | Sequence 10, Appl | C 960 | 9.4 | 32.4 | 20 | 3 | US-08-777-266A-9    | Sequence 9, Appl   |
| C 888 | 9.4 | 32.4 | 56 | 2 | US-08-976-413A-259  | Sequence 259, App | C 961 | 9.4 | 32.4 | 20 | 3 | US-09-287-796-88    | Sequence 88, Appl  |
| C 889 | 9.4 | 32.4 | 57 | 2 | US-08-465-591A-19   | Sequence 19, Appl | C 962 | 9.4 | 32.4 | 20 | 3 | US-09-287-796-88    | Sequence 88, Appl  |
| C 890 | 9.4 | 32.4 | 57 | 2 | US-08-465-591A-19   | Sequence 19, Appl | C 963 | 9.4 | 32.4 | 20 | 3 | US-09-130-616-88    | Sequence 88, Appl  |
| C 891 | 9.4 | 32.4 | 57 | 2 | US-08-973-124-204   | Sequence 204, App | C 964 | 9.4 | 32.4 | 20 | 3 | US-09-130-616-88    | Sequence 88, Appl  |
| C 892 | 9.4 | 32.4 | 57 | 5 | PCT-US96-08014-204  | Sequence 204, App | C 965 | 9.4 | 32.4 | 20 | 3 | US-09-130-616-89    | Sequence 89, Appl  |
| C 893 | 9.4 | 32.4 | 58 | 4 | US-09-621-976-12180 | Sequence 12180, A | C 966 | 9.4 | 32.4 | 20 | 3 | US-09-560-594-49    | Sequence 49, Appl  |
| C 894 | 9.4 | 32.4 | 59 | 4 | US-09-532-419A-10   | Sequence 10, Appl | C 967 | 9.4 | 32.4 | 20 | 3 | US-09-180-437-38    | Sequence 38, Appl  |
| C 895 | 9.4 | 32.4 | 59 | 4 | US-09-532-419A-10   | Sequence 10, Appl | C 968 | 9.4 | 32.4 | 20 | 4 | US-09-378-718-5     | Sequence 5, Appl   |
| C 896 | 9.4 | 32.4 | 60 | 3 | US-09-237-712-66    | Sequence 66, Appl | C 969 | 9.4 | 32.4 | 20 | 4 | US-09-488-856A-29   | Sequence 29, Appl  |
| C 897 | 9.4 | 32.4 | 61 | 3 | US-08-593-455B-21   | Sequence 21, Appl | C 970 | 9.4 | 32.4 | 20 | 4 | US-09-326-186B-9    | Sequence 9, Appl   |
| C 898 | 9.4 | 32.4 | 61 | 3 | US-09-069-781B-21   | Sequence 21, Appl | C 971 | 9.4 | 32.4 | 20 | 4 | US-09-468-872-68    | Sequence 68, Appl  |
| C 899 | 9.4 | 32.4 | 61 | 4 | US-09-137-132-21    | Sequence 21, Appl | C 972 | 9.4 | 32.4 | 20 | 4 | US-09-354-151-16    | Sequence 16, Appl  |
| C 900 | 9.4 | 32.4 | 61 | 4 | US-08-864-544A-21   | Sequence 21, Appl | C 973 | 9.4 | 32.4 | 20 | 4 | US-09-527-030G-328  | Sequence 328, App  |
| C 901 | 9.4 | 32.4 | 61 | 4 | US-09-094-410-21    | Sequence 21, Appl | C 974 | 9.4 | 32.4 | 20 | 4 | US-09-527-030G-334  | Sequence 334, App  |
| C 902 | 9.4 | 32.4 | 61 | 4 | US-08-708-123D-21   | Sequence 21, Appl | C 975 | 9.4 | 32.4 | 20 | 4 | US-09-198-452A-408  | Sequence 2408, Ap  |
| C 903 | 9.4 | 32.4 | 61 | 4 | US-08-583-153A-21   | Sequence 21, Appl | C 976 | 9.4 | 32.4 | 20 | 4 | US-09-198-452A-4077 | Sequence 3077, Ap  |

977 9.2 31.7 20 4 US-09-162-622-12 Sequence 12, Appl  
978 9.2 31.7 20 4 US-09-509-015-12 Sequence 12, Appl  
979 9.2 31.7 20 5 PCT-US95-06160-1 Sequence 1, Appl  
980 9.2 31.7 20 5 PCT-US96-08235-12 Sequence 12, Appl  
981 9.2 31.7 21 1 US-08-832-883-78 Sequence 78, Appl  
982 9.2 31.7 21 2 US-08-832-877-78 Sequence 78, Appl  
983 9.2 31.7 21 3 US-09-114-825-4 Sequence 4, Appl  
984 9.2 31.7 21 3 US-09-114-825-5 Sequence 5, Appl  
985 9.2 31.7 21 4 US-09-485-737B-50 Sequence 50, Appl  
986 9.2 31.7 21 4 US-09-593-012-196 Sequence 196, App  
987 9.2 31.7 21 4 US-09-422-978-6777 Sequence 6777, Ap  
988 9.2 31.7 21 4 US-09-422-978-7947 Sequence 7947, Ap  
989 9.2 31.7 21 4 US-09-422-978-10532 Sequence 10532, A  
990 9.2 31.7 21 4 US-09-422-978-11518 Sequence 11518, A  
991 9.2 31.7 22 2 US-09-044-506A-32 Sequence 32, Appl  
992 9.2 31.7 22 2 US-09-336-946B-33 Sequence 33, Appl  
993 9.2 31.7 23 2 US-08-975-902-44 Sequence 44, Appl  
994 9.2 31.7 23 3 US-09-251-565-44 Sequence 44, Appl  
995 9.2 31.7 23 3 US-09-254-733-14 Sequence 14, Appl  
996 9.2 31.7 23 3 US-09-316-083-5 Sequence 5, Appl  
997 9.2 31.7 23 4 US-09-933-700-5 Sequence 5, Appl  
998 9.2 31.7 24 1 US-08-242-680-4 Sequence 4, Appl  
999 9.2 31.7 24 2 US-08-464-257-5 Sequence 5, Appl  
1000 9.2 31.7 24 2 US-08-653-382A-4 Sequence 4, Appl

ALIGNMENTS

RESULT 1  
US-08-956-171E-2762  
; Sequence 2762, Application US/08956171E  
; Patent No. 6593114  
; GENERAL INFORMATION:  
; APPLICANT: Charles Kunsch  
; Gil H. Choi  
; Patrick S. Dillon  
; Craig A. Rosen  
; Steven C. Barash  
; Michael R. Fannon  
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences  
; NUMBER OF SEQUENCES: 5256  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: Maryland  
; COUNTRY: USA  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
; COMPUTER: HP Vectra 486/33  
; OPERATING SYSTEM: MSDOS version 6.2  
; SOFTWARE: ASCII Text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/956,171E  
; FILING DATE: 20-Oct-1997  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/009,861  
; FILING DATE: January 5, 1996  
; APPLICATION NUMBER: 08/781,986  
; FILING DATE: January 3, 1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mark J. Hyman  
; REGISTRATION NUMBER: 46,789  
; REFERENCE/DOCKET NUMBER: PB248P1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (240) 314-1224  
; TELEFAX: (301) 309-8439  
; INFORMATION FOR SEQ ID NO: 2762:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 68 base pairs

; TYPE: nucleic acid  
; STRANDEDNESS: Double  
; TOPOLOGY: linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 2762:  
US-08-956-171E-2762  
Query Match 44.1%; Score 12.8; DB 4; Length 68;  
Best Local Similarity 47.6%; Pred. No. 1.7e+02;  
Matches 10; Conservative 4; Mismatches 7; Indels 0; Gaps 0;  
Qy 5 AUNCUTUNNGUAGCCCNANG 25  
| : : : : :  
Db 3 ATCCTGTCTTAAGCCGACG 23  
| : : : : :  
RESULT 2  
5258283-10  
; Patent No. 5258283  
; APPLICANT: FRAZIER, MARVIN E.; MALLAVIA, LOUIS P.; SAMUEL,  
; JAMES E.; BACA, OSWALD G.  
; TITLE OF INVENTION: DETECTION AND DIFFERENTIATION OF COXIELLA  
; BURNETII IN BIOLOGICAL FLUIDS  
; NUMBER OF SEQUENCES: 17  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/425,856  
; FILING DATE: 23-OCT-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 927,779  
; FILING DATE: 05-NOV-1986  
; APPLICATION NUMBER: 795,207  
; FILING DATE: 05-NOV-1985  
; SEQ ID NO:10:  
; LENGTH: 27  
5258283-10  
Query Match 42.1%; Score 12.2; DB 6; Length 27;  
Best Local Similarity 40.9%; Pred. No. 3.1e+02;  
Matches 9; Conservative 5; Mismatches 8; Indels 0; Gaps 0;  
Qy 4 GAUNCUTUNNGUAGCCCNANG 25  
| : : : : :  
Db 4 GGTCTTTTGAATAAGCCCAATG 25  
| : : : : :  
RESULT 3  
US-08-410-654B-30  
; Sequence 30, Application US/08410654B  
; Patent No. 5833976  
; GENERAL INFORMATION:  
; APPLICANT: Rene de Waal Malefyt  
; APPLICANT: Di-Hwei Hsu  
; APPLICANT: Anne O'Garra  
; APPLICANT: Hergen Spits  
; TITLE OF INVENTION: Use of Interleukin-10 to Treat  
; TITLE OF INVENTION: Septic Shock  
; NUMBER OF SEQUENCES: 61  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Schering-Plough Corporation  
; STREET: 2000 Galloping Hill Road  
; CITY: Kenilworth  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07033  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Macintosh  
; OPERATING SYSTEM: 7.5.3  
; SOFTWARE: Microsoft Word 5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/410,654B  
; FILING DATE: 24-MAR-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/229,854  
FILING DATE: 19-APR-1994  
APPLICATION NUMBER: US 07/926,853  
FILING DATE: 06-AUG-1992  
APPLICATION NUMBER: US 07/742,129  
FILING DATE: 06-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Foulke, Cynthia L.  
REGISTRATION NUMBER: 32,364  
REFERENCE/DOCKET NUMBER: DX0221KQ1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 908-298-2987  
TELEFAX: 908-298-5388  
INFORMATION FOR SEQ ID NO: 30:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 69 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (oligonucleotide)  
US-08-410-854B-30

Query Match 42.1%; Score 12.2; DB 2; Length 69;  
Best Local Similarity 43.5%; Pred. No. 3.8e+02;  
Matches 10; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 5 AUNCUUNNGUAGCCCNANGNG 27  
| : : : : :  
Db 11 ATGCCTTTAATAAGCTCCAAGAG 33

## RESULT 4

US-08-474-851-30  
Sequence 30, Application US/08474851  
Patent No. 5837232  
GENERAL INFORMATION:  
APPLICANT: Rene de Waal Malefyt  
APPLICANT: Di-Hwei Hsu  
APPLICANT: Anne O'Garra  
APPLICANT: Hergen Spits  
TITLE OF INVENTION: Use of An Interleukin-10 Antagonist to Treat  
TITLE OF INVENTION: A B Cell Mediated Autoimmune Disorder  
NUMBER OF SEQUENCES: 61  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Schering-Plough Corporation  
STREET: 2000 Galloping Hill Road  
CITY: Kenilworth  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07033  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Macintosh  
OPERATING SYSTEM: 7.5.3  
SOFTWARE: Microsoft Word 6.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/474,851  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/410,654  
FILING DATE: 24-MAR-1995  
APPLICATION NUMBER: US 08/229,854  
FILING DATE: 19-APR-1994  
APPLICATION NUMBER: US 07/926,853  
FILING DATE: 06-AUG-1992  
APPLICATION NUMBER: US 07/742,129  
FILING DATE: 06-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Foulke, Cynthia L.  
REGISTRATION NUMBER: 32,364  
REFERENCE/DOCKET NUMBER: DX0221KQ1GD  
TELECOMMUNICATION INFORMATION:

TELEPHONE: 908-298-2987  
TELEFAX: 908-298-5388  
INFORMATION FOR SEQ ID NO: 30:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 69 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (oligonucleotide)  
US-08-474-851-30

Query Match 42.1%; Score 12.2; DB 2; Length 69;  
Best Local Similarity 43.5%; Pred. No. 3.8e+02;  
Matches 10; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 5 AUNCUUNNGUAGCCCNANGNG 27  
| : : : : :  
Db 11 ATGCCTTTAATAAGCTCCAAGAG 33

## RESULT 5

US-08-481-560-30  
Sequence 30, Application US/08481560  
Patent No. 5837293  
GENERAL INFORMATION:  
APPLICANT: Rene de Waal Malefyt  
APPLICANT: Di-Hwei Hsu  
APPLICANT: Anne O'Garra  
APPLICANT: Hergen Spits  
TITLE OF INVENTION: Use of Interleukin-10 to Modulate  
TITLE OF INVENTION: Inflammation or T-Cell Mediated  
NUMBER OF SEQUENCES: 61  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Schering-Plough Corporation  
STREET: 2000 Galloping Hill Road  
CITY: Kenilworth  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07033  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Macintosh  
OPERATING SYSTEM: 7.5.3  
SOFTWARE: Microsoft Word 6.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/481,560  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/410,654  
FILING DATE: 24-MAR-1995  
APPLICATION NUMBER: US 08/229,854  
FILING DATE: 19-APR-1994  
APPLICATION NUMBER: US 07/926,853  
FILING DATE: 06-AUG-1992  
APPLICATION NUMBER: US 07/742,129  
FILING DATE: 06-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Foulke, Cynthia L.  
REGISTRATION NUMBER: 32,364  
REFERENCE/DOCKET NUMBER: DX0221KQ1GC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 908-298-2987  
TELEFAX: 908-298-5388  
INFORMATION FOR SEQ ID NO: 30:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 69 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (oligonucleotide)  
US-08-481-560-30



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; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..36
; OTHER INFORMATION: /note="Nucleotides 5 through 36 are complementary to nucleotides 5 through 36"
US-08-218-369-15

Query Match 40.0%; Score 11.6; DB 4; Length 36;
Best Local Similarity 41.7%; Pred No. 7.6e+02;
Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 4 GAUNCUUNNGUAGCCCNANGNG 27
DB 10 GAAGCTTTAGGTGGGGCCCATGAG 33
||::||:|||||
10 GAAGCTTTAGGTGGGGCCCATGAG 33

RESULT 10
US-09-904-599A-7/c
; Sequence 7, Application US/09904599A
; Patent No. 6683170
; GENERAL INFORMATION:
; APPLICANT: Curiel, David T.,
; APPLICANT: Engler, Jeffrey A.
; TITLE OF INVENTION: Ligands Added to Adenovirus Fiber
; FILE REFERENCE: D5839/D
; CURRENT APPLICATION NUMBER: US/09/904,599A
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 08/218,369
; PRIOR FILING DATE: 1994-03-28
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 7
; LENGTH: 36
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence coding for streptavidin mimic
; OTHER INFORMATION: that binds biotin nucleotide sequence
US-09-904-599A-7

Query Match 40.0%; Score 11.6; DB 4; Length 36;
Best Local Similarity 41.7%; Pred. No. 7.6e+02;
Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 4 GAUNCUUNNGUAGCCCNANGNG 27
DB 31 GAAGCTTTAGGTGGGGCCCATGAG 8
||::||:|||||
31 GAAGCTTTAGGTGGGGCCCATGAG 8

RESULT 11
PCT-US95-03742-7/c
; Sequence 7, Application PC/TUS9503742
; GENERAL INFORMATION:
; APPLICANT: The UAB Research Foundation
; TITLE OF INVENTION: Ligands Added to Adenovirus Fiber
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/03742
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:

```



```

; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: IG1101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..36
; OTHER INFORMATION: /note= "Nucleotide sequence
; OTHER INFORMATION: encoding a streptavidin mimic that binds biotin."
PCT-US95-03742-7

Query Match 40.0%; Score 11.6; DB 5; Length 36;
Best Local Similarity 41.7%; Pred. No. 7.6e+02;
Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 4 GAUNCUUUNNGUAAGCCCNANGNG 27
Db 31 GAAGCTTTAGTGGGGCCCATGAG 8

RESULT 12
PCT-US95-03742-15
; Sequence 15, Application PC/TUS9503742
; GENERAL INFORMATION:
; APPLICANT: The UAB Research Foundation
; TITLE OF INVENTION: Ligands Added to Adenovirus Fiber
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/03742
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: IG1101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: misc feature

```

```

; LOCATION: 1..36
; OTHER INFORMATION: /note= "Nucleotides 5 through 36
; OTHER INFORMATION: are complementary to nucleotides 5 through 36 of
; OTHER INFORMATION: Sequence ID No. 7."
PCT-US95-03742-15

Query Match 40.0%; Score 11.6; DB 5; Length 36;
Best Local Similarity 41.7%; Pred. No. 7.6e+02;
Matches 10; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 4 GAUNCUUUNNGUAAGCCCNANGNG 27
Db 10 GAAGCTTTAGTGGGGCCCATGAG 33

RESULT 13
US-09-619-213B-45/c
; Sequence 45, Application US/09619213B
; Patent No. 6458539
; GENERAL INFORMATION:
; APPLICANT: Gold, Larry
; APPLICANT: Smith, Jonathan Drew
; APPLICANT: Koch, Tad
; APPLICANT: Golden, Mace
; TITLE OF INVENTION: Photoselection of Nucleic Acid Ligands
; FILE REFERENCE: NEX10-5
; CURRENT APPLICATION NUMBER: US/09/619,213B
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/459,553
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 09/093,293
; PRIOR FILING DATE: 1998-06-08
; PRIOR APPLICATION NUMBER: 08/612,895
; PRIOR FILING DATE: 1996-03-08
; PRIOR APPLICATION NUMBER: 08/123,935
; PRIOR FILING DATE: 1993-09-17
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 45
; LENGTH: 61
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
; OTHER INFORMATION: Ligand
; NAME/KEY: modified base
; LOCATION: (1)..(61)
; OTHER INFORMATION: All T's are 5-bromouracil
US-09-619-213B-45

Query Match 40.0%; Score 11.6; DB 4; Length 61;
Best Local Similarity 45.8%; Pred. No. 8.6e+02;
Matches 11; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 4 GAUNCUUUNNGUAAGCCCNANGNG 27
Db 42 GATACATATGACAGCCCATGAG 19

RESULT 14
US-09-849-069-37/c
; Sequence 37, Application US/09849069
; Patent No. 6630306
; GENERAL INFORMATION:
; APPLICANT: Ronald R. Breaker
; TITLE OF INVENTION: Bioreactive Allosteric Polynucleotides
; FILE REFERENCE: OCR-794.CIP
; CURRENT APPLICATION NUMBER: US/09/849,069
; CURRENT FILING DATE: 2001-05-07
; PRIOR APPLICATION NUMBER: US 09/331,809
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: MS-DOS

```

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; SEQ ID NO 37
; LENGTH: 65
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: DNA with 3 cleavage sites
US-09-849-069-37

Query Match      39.3%; Score 11.4; DB 4; Length 65;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY      10 UUNNGUAGCCCNANGNG 27
DB      51 TTCGTAAGCCACATGAG 34

RESULT 15
US-08-741-981-28/c
; Sequence 28, Application US/08741881
; Patent No. 5789245
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Ibanez, Carlos E.
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; APPLICANT: Belli, Barbara A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/741.881
; FILING DATE: 30-OCT-1996
; CLASSIFICATION: 435
; NAME: Mcmasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423C6 / 1146.007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-741-881-28

Query Match      38.6%; Score 11.2; DB 1; Length 25;
Best Local Similarity 36.4%; Pred. No. 1.2e+03;
Matches 8; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY      6 UUNGUAGCCCNANGNG 27
DB      24 TCCTTAGGTAGCCGTACAAG 3

RESULT 16
US-08-739-158-28/c
; Sequence 28, Application US/08739167
; Patent No. 5843723
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Ibanez, Carlos E.
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; APPLICANT: Belli, Barbara A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS AND ALPHAVIRUS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
```

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; Sequence 28, Application US/08739158
; Patent No. 5814482
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/739,158
; FILING DATE: 30-OCT-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcmasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049.423D3 / 1146.012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-739-158-28

Query Match      38.6%; Score 11.2; DB 1; Length 25;
Best Local Similarity 36.4%; Pred. No. 1.2e+03;
Matches 8; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY      6 UUNGUAGCCCNANGNG 27
DB      24 TCCTTAGGTAGCCGTACAAG 3

RESULT 17
US-08-739-167-28/c
; Sequence 28, Application US/08739167
; Patent No. 5843723
; GENERAL INFORMATION:
; APPLICANT: Dubensky Jr, Thomas W
; APPLICANT: Polo, John M.
; APPLICANT: Ibanez, Carlos E.
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Driver, David A.
; APPLICANT: Belli, Barbara A.
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS AND ALPHAVIRUS
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/739,167  
; FILING DATE: 30-OCT-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McMasters, David D.  
; REGISTRATION NUMBER: 33,963  
; REFERENCE/DOCKET NUMBER: 930049.423C7 / 1146.008  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 28:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 25 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-739-167-28  
  
Query Match 38.6%; Score 11.2; DB 2; Length 25;  
Best Local Similarity 36.4%; Pred. No. 1.2e+03;  
Matches 8; Conservative 5; Mismatches 9; Indels 0; Gaps 0;  
  
QY 6 UNCUUNNGUAGCCNANGNG 27  
Db 24 TCCTTTAGGTAGCGGTACAAG 3  
  
RESULT 18  
US-08-404-796-28/c  
; Sequence 28, Application US/08404796  
; Patent No. 6015686  
; GENERAL INFORMATION:  
; APPLICANT: Dubensky Jr, Thomas W  
; APPLICANT: Polo, John M.  
; APPLICANT: Ibanez, Carlos E.  
; APPLICANT: Chang, Stephen M.W.  
; APPLICANT: Jolly, Douglas J.  
; APPLICANT: Driver, David A.  
; APPLICANT: Belli, Barbara A.  
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS  
; NUMBER OF SEQUENCES: 128  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED and BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: US  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/739,167  
; FILING DATE: 16-SEP-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/404,796  
; FILING DATE: 15-MAR-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McMasters, David D.  
; REGISTRATION NUMBER: 33,963  
; REFERENCE/DOCKET NUMBER: 930049.423C5 / 1146.006  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 28:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 25 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-404-796-28

US-08-404-796-28  
Query Match 38.6%; Score 11.2; DB 3; Length 25;  
Best Local Similarity 36.4%; Pred. No. 1.2e+03;  
Matches 8; Conservative 5; Mismatches 9; Indels 0; Gaps 0;  
  
QY 6 UNCUUNNGUAGCCNANGNG 27  
Db 24 TCCTTTAGGTAGCGGTACAAG 3  
  
RESULT 19  
US-08-931-869-28/c  
; Sequence 28, Application US/08931869  
; Patent No. 6015694  
; GENERAL INFORMATION:  
; APPLICANT: Dubensky Jr, Thomas W  
; APPLICANT: Polo, John M.  
; APPLICANT: Ibanez, Carlos E.  
; APPLICANT: Chang, Stephen M.W.  
; APPLICANT: Jolly, Douglas J.  
; APPLICANT: Driver, David A.  
; APPLICANT: Belli, Barbara A.  
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS  
; NUMBER OF SEQUENCES: 128  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED and BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: US  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/931,869  
; FILING DATE: 16-SEP-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/404,796  
; FILING DATE: 15-MAR-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McMasters, David D.  
; REGISTRATION NUMBER: 33,963  
; REFERENCE/DOCKET NUMBER: 930049.423C5 / 1146.006  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 28:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 25 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-931-869-28  
  
Query Match 38.6%; Score 11.2; DB 3; Length 25;  
Best Local Similarity 36.4%; Pred. No. 1.2e+03;  
Matches 8; Conservative 5; Mismatches 9; Indels 0; Gaps 0;  
  
QY 6 UNCUUNNGUAGCCNANGNG 27  
Db 24 TCCTTTAGGTAGCGGTACAAG 3  
  
RESULT 20  
US-09-350-399-28/c  
; Sequence 28, Application US/09350399  
; Patent No. 6342372  
; GENERAL INFORMATION:

APPLICANT: Dubensky Jr, Thomas W  
Polo, John M.  
Jolly, Douglas J.  
Driver, David A.  
TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS  
NUMBER OF SEQUENCES: 128  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED and BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/350,399  
FILING DATE: 08-Jul-1999  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: McMaisters, David D.  
REGISTRATION NUMBER: 33,963  
REFERENCE/DOCKET NUMBER: 930049.423D1 / 1146.010  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 25 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 28:  
US-09-350-399-28  
Query Match 38.6%; Score 11.2; DB 4; Length 25;  
Best Local Similarity 36.4%; Pred. No. 1.2e+03;  
Matches 8; Conservative 5; Mismatches 9; Indels 0; Gaps 0;  
QY 6 UCUUUNGUAGCCCNANGNG 27  
Db 24 TCCTTAGTTAGCGGTACAAG 3  
RESULT 21  
US-09-236-140A-28/c  
Sequence 28, Application US/09236140A  
Patent No. 6376236  
GENERAL INFORMATION:  
APPLICANT: Dubensky Jr, Thomas W  
Polo, John M.  
Ibanez, Carlos E.  
Chang, Stephen M.W.  
Jolly, Douglas J.  
Driver, David A.  
Belli, Barbara A.  
TITLE OF INVENTION: RECOMBINANT ALPHAVIRUS PARTICLES  
NUMBER OF SEQUENCES: 124  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OPPENHEIMER WOLFF & DONNELLY  
STREET: 840 NEWPORT CENTER DRIVE, SUITE 700  
CITY: NEWPORT BEACH  
STATE: CALIFORNIA  
COUNTRY: US  
ZIP: 92660  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/236,140A  
FILING DATE: 22-Jan-1999  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Cullman, Louis C.  
REGISTRATION NUMBER: 39,645  
REFERENCE/DOCKET NUMBER: 20263.332 / 1146.020  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (949) 823-6000  
TELEFAX: (949) 823-6100  
INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 25 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 28:  
US-09-236-140A-28  
Query Match 38.6%; Score 11.2; DB 4; Length 25;  
Best Local Similarity 36.4%; Pred. No. 1.2e+03;  
Matches 8; Conservative 5; Mismatches 9; Indels 0; Gaps 0;  
QY 6 UCUUUNGUAGCCCNANGNG 27  
Db 24 TCCTTAGTTAGCGGTACAAG 3  
RESULT 22  
US-08-741-881-29  
Sequence 29, Application US/08741881  
Patent No. 5789245  
GENERAL INFORMATION:  
APPLICANT: Dubensky Jr, Thomas W  
Polo, John M.  
Ibanez, Carlos E.  
Chang, Stephen M.W.  
Jolly, Douglas J.  
Driver, David A.  
Belli, Barbara A.  
TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS  
NUMBER OF SEQUENCES: 128  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED and BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/741,881  
FILING DATE: 30-OCT-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: McMaisters, David D.  
REGISTRATION NUMBER: 33,963  
REFERENCE/DOCKET NUMBER: 930049.423C6 / 1146.007  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 33 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-741-881-29

Query Match 38.6%; Score 11.2; DB 1; Length 33;  
Best Local Similarity 36.4%; Pred. No. 1.3e+03;  
Matches 8; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

Qy 6 UCUUUNNGUAGCCCNANGNG 27  
Db 6 TCCTTTAGTTAGCCGTACAG 27

## RESULT 23

US-08-739-158-29  
; Sequence 29, Application US/08739158  
; Patent No. 581482  
; GENERAL INFORMATION:  
; APPLICANT: Dubensky Jr, Thomas W  
; APPLICANT: Polo, John M.  
; APPLICANT: Jolly, Douglas J.  
; APPLICANT: Driver, David A.  
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS  
; NUMBER OF SEQUENCES: 128  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED and BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; City: Seattle  
; STATE: Washington  
; COUNTRY: US  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/739,158  
; FILING DATE: 30-OCT-1996  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McMasters, David D.  
; REGISTRATION NUMBER: 33,963  
; REFERENCE/DOCKET NUMBER: 930049.423D3 / 1146.012  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 29:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 33 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-739-158-29

Query Match 38.6%; Score 11.2; DB 1; Length 33;  
Best Local Similarity 36.4%; Pred. No. 1.3e+03;  
Matches 8; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

Qy 6 UCUUUNNGUAGCCCNANGNG 27  
Db 6 TCCTTTAGTTAGCCGTACAG 27

## RESULT 24

US-08-739-167-29  
; Sequence 29, Application US/08739167  
; Patent No. 5843723  
; GENERAL INFORMATION:  
; APPLICANT: Dubensky Jr, Thomas W  
; APPLICANT: Polo, John M.  
; APPLICANT: Ibanez, Carlos E.  
; APPLICANT: Chang, Stephen M.W.  
; APPLICANT: Jolly, Douglas J.  
; APPLICANT: Driver, David A.  
; APPLICANT: Belli, Barbara A.  
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS  
; NUMBER OF SEQUENCES: 128  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED and BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; City: Seattle  
; STATE: Washington  
; COUNTRY: US  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/739,167  
; FILING DATE: 30-OCT-1996  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McMasters, David D.  
; REGISTRATION NUMBER: 33,963  
; REFERENCE/DOCKET NUMBER: 930049.423D3 / 1146.012  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 29:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 33 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-739-167-29

Query Match 38.6%; Score 11.2; DB 1; Length 33;  
Best Local Similarity 36.4%; Pred. No. 1.3e+03;  
Matches 8; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

Qy 6 UCUUUNNGUAGCCCNANGNG 27  
Db 6 TCCTTTAGTTAGCCGTACAG 27

## RESULT 25

US-08-404-796-29  
; Sequence 29, Application US/08404796  
; Patent No. 6015686  
; GENERAL INFORMATION:  
; APPLICANT: Dubensky Jr, Thomas W  
; APPLICANT: Polo, John M.  
; APPLICANT: Ibanez, Carlos E.  
; APPLICANT: Chang, Stephen M.W.  
; APPLICANT: Jolly, Douglas J.  
; APPLICANT: Driver, David A.  
; APPLICANT: Belli, Barbara A.  
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS  
; NUMBER OF SEQUENCES: 128  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED and BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; City: Seattle  
; STATE: Washington  
; COUNTRY: US  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/404,796  
; FILING DATE: 15-MAR-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McMasters, David D.  
; REGISTRATION NUMBER: 33,963  
; REFERENCE/DOCKET NUMBER: 930049.423C7 / 1146.008  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 29:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 33 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-404-796-29

Query Match 38.6%; Score 11.2; DB 1; Length 33;  
Best Local Similarity 36.4%; Pred. No. 1.3e+03;  
Matches 8; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

Qy 6 UCUUUNNGUAGCCCNANGNG 27  
Db 6 TCCTTTAGTTAGCCGTACAG 27

## RESULT 26

US-08-739-167-29  
; Sequence 29, Application US/08739167  
; Patent No. 5843723  
; GENERAL INFORMATION:  
; APPLICANT: Dubensky Jr, Thomas W  
; APPLICANT: Polo, John M.  
; APPLICANT: Ibanez, Carlos E.  
; APPLICANT: Chang, Stephen M.W.  
; APPLICANT: Jolly, Douglas J.  
; APPLICANT: Driver, David A.  
; APPLICANT: Belli, Barbara A.  
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS  
; NUMBER OF SEQUENCES: 128  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED and BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; City: Seattle  
; STATE: Washington  
; COUNTRY: US  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/404,796  
; FILING DATE: 15-MAR-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McMasters, David D.  
; REGISTRATION NUMBER: 33,963  
; REFERENCE/DOCKET NUMBER: 930049.423C7 / 1146.008  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 29:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 33 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-739-167-29

Query Match 38.6%; Score 11.2; DB 1; Length 33;  
Best Local Similarity 36.4%; Pred. No. 1.3e+03;  
Matches 8; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

Qy 6 UCUUUNNGUAGCCCNANGNG 27  
Db 6 TCCTTTAGTTAGCCGTACAG 27

; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS AND ALPHAVIRUS  
; NUMBER OF SEQUENCES: 128  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED and BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; City: Seattle  
; STATE: Washington  
; COUNTRY: US  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/739,167  
; FILING DATE: 30-OCT-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McMasters, David D.  
; REGISTRATION NUMBER: 33,963  
; REFERENCE/DOCKET NUMBER: 930049.423C7 / 1146.008  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 29:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 33 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-739-167-29

Query Match 38.6%; Score 11.2; DB 2; Length 33;  
Best Local Similarity 36.4%; Pred. No. 1.3e+03;  
Matches 8; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

Qy 6 UCUUUNNGUAGCCCNANGNG 27  
Db 6 TCCTTTAGTTAGCCGTACAG 27

## RESULT 27

US-08-404-796-29  
; Sequence 29, Application US/08404796  
; Patent No. 6015686  
; GENERAL INFORMATION:  
; APPLICANT: Dubensky Jr, Thomas W  
; APPLICANT: Polo, John M.  
; APPLICANT: Ibanez, Carlos E.  
; APPLICANT: Chang, Stephen M.W.  
; APPLICANT: Jolly, Douglas J.  
; APPLICANT: Driver, David A.  
; APPLICANT: Belli, Barbara A.  
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS  
; NUMBER OF SEQUENCES: 128  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED and BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; City: Seattle  
; STATE: Washington  
; COUNTRY: US  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/739,167  
; FILING DATE: 30-OCT-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McMasters, David D.  
; REGISTRATION NUMBER: 33,963  
; REFERENCE/DOCKET NUMBER: 930049.423C7 / 1146.008  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 29:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 33 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-739-167-29

Query Match 38.6%; Score 11.2; DB 2; Length 33;  
Best Local Similarity 36.4%; Pred. No. 1.3e+03;  
Matches 8; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

Qy 6 UCUUUNNGUAGCCCNANGNG 27  
Db 6 TCCTTTAGTTAGCCGTACAG 27

## RESULT 28

US-08-404-796-29  
; Sequence 29, Application US/08404796  
; Patent No. 6015686  
; GENERAL INFORMATION:  
; APPLICANT: Dubensky Jr, Thomas W  
; APPLICANT: Polo, John M.  
; APPLICANT: Ibanez, Carlos E.  
; APPLICANT: Chang, Stephen M.W.  
; APPLICANT: Jolly, Douglas J.  
; APPLICANT: Driver, David A.  
; APPLICANT: Belli, Barbara A.  
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS  
; NUMBER OF SEQUENCES: 128  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED and BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; City: Seattle  
; STATE: Washington  
; COUNTRY: US  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/404,796  
; FILING DATE: 15-MAR-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McMasters, David D.  
; REGISTRATION NUMBER: 33,963  
; REFERENCE/DOCKET NUMBER: 930049.423C7 / 1146.008  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 29:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 33 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-404-796-29

Query Match 38.6%; Score 11.2; DB 2; Length 33;  
Best Local Similarity 36.4%; Pred. No. 1.3e+03;  
Matches 8; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

Qy 6 UCUUUNNGUAGCCCNANGNG 27  
Db 6 TCCTTTAGTTAGCCGTACAG 27

## RESULT 29

US-08-739-167-29  
; Sequence 29, Application US/08739167  
; Patent No. 5843723  
; GENERAL INFORMATION:  
; APPLICANT: Dubensky Jr, Thomas W  
; APPLICANT: Polo, John M.  
; APPLICANT: Ibanez, Carlos E.  
; APPLICANT: Chang, Stephen M.W.  
; APPLICANT: Jolly, Douglas J.  
; APPLICANT: Driver, David A.  
; APPLICANT: Belli, Barbara A.  
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS  
; NUMBER OF SEQUENCES: 128  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED and BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; City: Seattle  
; STATE: Washington  
; COUNTRY: US  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/404,796  
; FILING DATE: 15-MAR-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McMasters, David D.  
; REGISTRATION NUMBER: 33,963  
; REFERENCE/DOCKET NUMBER: 930049.423C7 / 1146.008  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 29:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 33 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-739-167-29

Query Match 38.6%; Score 11.2; DB 2; Length 33;  
Best Local Similarity 36.4%; Pred. No. 1.3e+03;  
Matches 8; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

Qy 6 UCUUUNNGUAGCCCNANGNG 27  
Db 6 TCCTTTAGTTAGCCGTACAG 27

NAME: Mcmasters, David D.  
REGISTRATION NUMBER: 33,963  
REFERENCE/DOCKET NUMBER: 930049.423C5 / 1146.006  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 33 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-404-796-29

Query Match 38.6%; Score 11.2; DB 3; Length 33;  
Best Local Similarity 36.4%; Pred. No. 1.3e+03;  
Matches 8; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 6 UNCUNNGUAGCCCNANGNG 27  
Db 6 TCCTTTAGGTAGCGTACAAG 27

RESULT 26  
US-08-931-869-29  
; Sequence 29, Application US/08931869  
; Patent No. 6015694  
; GENERAL INFORMATION:  
; APPLICANT: Dubensky Jr, Thomas W  
; APPLICANT: Polo, John M.  
; APPLICANT: Ibanez, Carlos E.  
; APPLICANT: Chang, Stephen M.W.  
; APPLICANT: Jolly, Douglas J.  
; APPLICANT: Driver, David A.  
; APPLICANT: Belli, Barbara A.  
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS  
; NUMBER OF SEQUENCES: 128  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED and BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: US  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/931,869  
; FILING DATE: 16-SEP-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/404,796  
; FILING DATE: 15-MAR-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mcmasters, David D.  
; REGISTRATION NUMBER: 33,963  
; REFERENCE/DOCKET NUMBER: 930049.423C5 / 1146.006  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 29:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 33 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-931-869-29

Query Match 38.6%; Score 11.2; DB 3; Length 33;  
Best Local Similarity 36.4%; Pred. No. 1.3e+03;

Matches 8; Conservative 5; Mismatches 9; Indels 0; Gaps 0;  
QY 6 UNCUNNGUAGCCCNANGNG 27  
Db 6 TCCTTTAGGTAGCGTACAAG 27

RESULT 27  
US-09-350-399-29  
; Sequence 29, Application US/09350399  
; Patent No. 6342372  
; GENERAL INFORMATION:  
; APPLICANT: Dubensky Jr, Thomas W  
; APPLICANT: Polo, John M.  
; APPLICANT: Jolly, Douglas J.  
; APPLICANT: Driver, David A.

TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS  
NUMBER OF SEQUENCES: 128  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED and BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/350,399  
FILING DATE: 08-Jul-1999  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Mcmasters, David D.  
REGISTRATION NUMBER: 33,963  
REFERENCE/DOCKET NUMBER: 930049.423D1 / 1146.010  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 33 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 29:  
US-09-350-399-29

Query Match 38.6%; Score 11.2; DB 4; Length 33;  
Best Local Similarity 36.4%; Pred. No. 1.3e+03;  
Matches 8; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 6 UNCUNNGUAGCCCNANGNG 27  
Db 6 TCCTTTAGGTAGCGTACAAG 27

RESULT 28  
US-09-236-140A-29  
; Sequence 29, Application US/09236140A  
; Patent No. 6376236  
; GENERAL INFORMATION:  
; APPLICANT: Dubensky Jr, Thomas W  
; APPLICANT: Polo, John M.  
; APPLICANT: Ibanez, Carlos E.  
; APPLICANT: Chang, Stephen M.W.  
; APPLICANT: Jolly, Douglas J.  
; APPLICANT: Driver, David A.  
; APPLICANT: Belli, Barbara A.  
; TITLE OF INVENTION: RECOMBINANT ALPHAVIRUS PARTICLES  
; NUMBER OF SEQUENCES: 124

```
/
/
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: OPPENHEIMER WOLFF & DONNELLY
/ STREET: 840 NEWPORT CENTER DRIVE, SUITE 700
/ CITY: NEWPORT BEACH
/ STATE: CALIFORNIA
/ COUNTRY: US
/ ZIP: 92660
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/
/ CURRENT APPLICATION DATA: US/09/236,140A
/ APPLICATION NUMBER: US/09/236,140A
/ FILING DATE: 22-Jan-1999
/ CLASSIFICATION: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Cullman, Louis C.
/ REGISTRATION NUMBER: 39,645
/ REFERENCE/DOCKET NUMBER: 20263.332 / 1146.020
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (949) 823.6000
/ TELEFAX: (949) 823.6100
/
/ INFORMATION FOR SEQ ID NO: 29:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 33 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/
/ -SEQUENCE DESCRIPTION: SEQ ID NO: 29:
/
/ US-09-236-140A-29
/
/ Query Match 38.6%; Score 11.2; DB 4; Length 33;
/ Best Local Similarity 36.4%; Pred. No. 1.3e+03;
/ Matches 8; Conservative 5; Mismatches 9; Indels 0; Gaps 0;
/
/ QY 6 UCUUUNNGUAGCCCNANGNG 27
/ Db 6 TCCTTTAGGTAGCCGTACAG 27
/
/ RESULT 29
/ US-08-642-045B-17/c
/ Sequence 17, Application US/08642045B
/ Patent No. 5851804
/
/ GENERAL INFORMATION:
/ APPLICANT: Snyder, Linda A.
/ APPLICANT: Satishchandran, C.
/ TITLE OF INVENTION: CHIMERIC KANAMYCIN RESISTANCE GENE
/ NUMBER OF SEQUENCES: 25
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5851804ris
/ STREET: One Liberty Place, 46th floor
/ CITY: Philadelphia
/ STATE: Pennsylvania
/ COUNTRY: USA
/ ZIP: 19103
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: WINDOWS
/ SOFTWARE: WordPerfect 6.0/5.1
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/642,045B
/ FILING DATE: 06-MAY-1996
/ CLASSIFICATION: 514
/ ATTORNEY/AGENT INFORMATION:
/ NAME: DeLuca, Mark
/ REGISTRATION NUMBER: 33,229
/ REFERENCE/DOCKET NUMBER: APOL-0262
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 215-568-3100
/ TELEFAX: 215-568-3439
/
/ INFORMATION FOR SEQ ID NO: 29:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 33 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA
/
/ US-08-642-045B-17
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/
/
/ INFORMATION FOR SEQ ID NO: 17:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 36 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA
/
/ US-08-642-045B-17
/
/ Query Match 38.6%; Score 11.2; DB 2; Length 36;
/ Best Local Similarity 40.9%; Pred. No. 1.3e+03;
/ Matches 9; Conservative 4; Mismatches 9; Indels 0; Gaps 0;
/
/ QY 6 UCUUUNNGUAGCCCNANGNG 27
/ Db 35 TGTTCAGTTAAGACCGACGCG 14
/
/ RESULT 30
/ US-08-852-268-17/c
/ Sequence 17, Application US/08852268
/ Patent No. 6143527
/
/ GENERAL INFORMATION:
/ APPLICANT: Pachuk, Catherine J.
/ APPLICANT: Samuel, Manoj
/ APPLICANT: Zurawski, John A.
/ APPLICANT: Satishchandran, C.
/ TITLE OF INVENTION: CHAIN REACTION CLONING
/ NUMBER OF SEQUENCES: 21
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6143527ris
/ STREET: One Liberty Place, 46th floor
/ CITY: Philadelphia
/ STATE: Pennsylvania
/ COUNTRY: USA
/ ZIP: 19103
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: WINDOWS
/ SOFTWARE: WordPerfect
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/852,268
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/642,045
/ FILING DATE: 06-MAY-1996
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: DeLuca, Mark
/ REGISTRATION NUMBER: 33,229
/ REFERENCE/DOCKET NUMBER: APOL-0265
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 215-568-3100
/ TELEFAX: 215-568-3439
/
/ INFORMATION FOR SEQ ID NO: 17:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 36 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA
/
/ US-08-852-268-17
/
/ Query Match 38.6%; Score 11.2; DB 3; Length 36;
/ Best Local Similarity 40.9%; Pred. No. 1.3e+03;
/ Matches 9; Conservative 4; Mismatches 9; Indels 0; Gaps 0;
/
/ QY 6 UCUUUNNGUAGCCCNANGNG 27
/ Db 35 TGTTCAGTTAAGACCGACGCG 14
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RESULT 31
US-09-571-774-2
; Sequence 2, Application US/09571774
; Patent No. 6479262
; GENERAL INFORMATION:
; APPLICANT: Delagrave, Simon
; TITLE OF INVENTION: Solid Phase Enzymatic Assembly of Polynucleotides
; FILE REFERENCE: HER-0005
; CURRENT APPLICATION NUMBER: US/09/571,774
; CURRENT FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 41
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer Oligonucleotide
US-09-571-774-2

Query Match      38.6%; Score 11.2; DB 4; Length 41;
Best Local Similarity 50.0%; Pred. No. 1.4e+03;
Matches 10; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy      4 GAUNCUUNNGUAGCCCA 23
|||:|:|:|:|:|:|:|:|:|:|
Db      16 GATTCCTCTGTTAGCCCA 35

RESULT 32
US-09-852-385-2
; Sequence 2, Application US/09852385
; Patent No. 6635453
; GENERAL INFORMATION:
; APPLICANT: Delagrave, Simon
; APPLICANT: Marrs, Barry
; TITLE OF INVENTION: Methods For The Enzymatic Assembly Of Polynucleotides And Identifi
; TITLE OF INVENTION: Of Polynucleotides Having Desired Characteristics
; FILE REFERENCE: HER-0042
; CURRENT APPLICATION NUMBER: US/09/852,385
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 09/571,774
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 41
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: No. 6635453el Sequence
US-09-852-385-2

Query Match      38.6%; Score 11.2; DB 4; Length 41;
Best Local Similarity 50.0%; Pred. No. 1.4e+03;
Matches 10; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy      4 GAUNCUUNNGUAGCCCA 23
|||:|:|:|:|:|:|:|:|:|:|
Db      16 GATTCCTCTGTTAGCCCA 35

RESULT 33
US-09-422-978-2842
; Sequence 2842, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
```

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FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 2842
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 99-19348-229 : polymorphic base T or C
US-09-422-978-2842

Query Match      38.6%; Score 11.2; DB 4; Length 47;
Best Local Similarity 55.0%; Pred. No. 1.4e+03;
Matches 11; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Qy      4 GAUNCUUNNGUAGCCCA 23
|||:|:|:|:|:|:|:|:|:|:|
Db      16 GAATCTATYAGCAGCCCTA 35

RESULT 34
US-09-310-463-6
; Sequence 6, Application US/09310463A
; Patent No. 6384203
; GENERAL INFORMATION:
; APPLICANT: Cosman, David J.
; APPLICANT: Anderson, Dirk M.
; APPLICANT: Borges, Luis
; TITLE OF INVENTION: Family of Immunoregulators Designated Leukocyte Immunoglobulin-
; TITLE OF INVENTION: Like Receptors (LIR)
; FILE REFERENCE: 2624-A
; CURRENT APPLICATION NUMBER: US/09/310,463A
; CURRENT FILING DATE: 1999-05-12
; EARLIER APPLICATION NUMBER: 08/842,248
; EARLIER FILING DATE: 1997-04-24
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 52
; TYPE: DNA
; ORGANISM: human
; OTHER INFORMATION:
US-09-310-463-6

Query Match      38.6%; Score 11.2; DB 4; Length 52;
Best Local Similarity 40.9%; Pred. No. 1.4e+03;
Matches 9; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

Qy      6 UNCUUNNGUAGCCCNANGNG 27
|||:|:|:|:|:|:|:|:|:|:|
Db      27 TTCCTTCTATAACCCCGAGGTG 48

RESULT 35
US-08-842-248A-6
; Sequence 6, Application US/08842248A
; Patent No. 6448035
; GENERAL INFORMATION:
; APPLICANT: Cosman, David J.
; TITLE OF INVENTION: Family of Immunoregulators Designated
; TITLE OF INVENTION: Leukocyte Immunoglobulin-Like Receptors (LIR)
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Janis C. Henry, Immunex Corporation
; STREET: 51 University Street
```



/ CITY: Seattle  
/ STATE: WA  
/ COUNTRY: US  
/ ZIP: 98101  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ OPERATING SYSTEM: IBM/PC Compatible  
/ SOFTWARE: Microsoft Word 7.0  
/ CURRENT APPLICATION DATA:  
/ TITLE OF INVENTION: Recombinant Equine Herpesvirus  
/ NUMBER OF SEQUENCES: 1.25  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/08/842,248A  
/ FILING DATE: April 24, 1997  
/ CLASSIFICATION: 536  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Henry, Janis C.  
/ REGISTRATION NUMBER: 34,347  
/ REFERENCE/DOCKET NUMBER: 2624  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: (206) 587-0430  
/ TELEFAX: (206) 233-0644  
/ TELEX: 756922  
/ INFORMATION FOR SEQ ID NO: 6:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 52 nucleotides  
/ TYPE: nucleic acid  
/ STRANDEDNESS: single  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: Oligonucleotide  
/ US-08-842-248A-6

Query Match 38.6%; Score 11.2; DB 4; Length 52;  
Best Local Similarity 40.9%; Pred. No. 1.4e+03;  
Matches 9; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 6 UNCUCUUNGUAGCCCNANG 27  
DB 27 TTCCTTCTATAACCCCGGTG 48

RESULT 36  
US-09-364-380-29  
/ Sequence 29, Application US/09364380A  
/ Patent No. 6171795  
/ GENERAL INFORMATION:  
/ APPLICANT: Korman, Alan J.  
/ APPLICANT: Gold, Larry  
/ TITLE OF INVENTION: Nucleic Acid Ligands to CD40Ligand  
/ FILE REFERENCE: NEX85  
/ CURRENT APPLICATION NUMBER: US/09/364,380A  
/ CURRENT FILING DATE: 1999-07-29  
/ NUMBER OF SEQ ID NOS: 33  
/ SOFTWARE: Patent Ver. 2.0  
/ SEQ ID NO 29  
/ LENGTH: 70  
/ TYPE: RNA  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
/ OTHER INFORMATION: Sequence  
/ FEATURE:  
/ NAME/KEY: modified base  
/ LOCATION: (1)..(70)  
/ OTHER INFORMATION: All pyrimidines are 2' F.  
/ US-09-364-380-29

Query Match 38.6%; Score 11.2; DB 3; Length 70;  
Best Local Similarity 61.9%; Pred. No. 1.5e+03;  
Matches 13; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 5 AUNCUCUUNGUAGCCCNANG 25  
DB 38 AUCAUUCUUGUAGCCCUACG 58

RESULT 37  
US-08-323-531-71/C  
/ Sequence 71, Application US/08323531  
/ Patent No. 5731189  
/ GENERAL INFORMATION:  
/ APPLICANT: Cochran Ph.D., Mark D  
/ TITLE OF INVENTION: Recombinant Equine Herpesvirus  
/ NUMBER OF SEQUENCES: 71  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: John P. White  
/ STREET: 30 Rockefeller Plaza  
/ CITY: New York  
/ STATE: New York  
/ COUNTRY: USA  
/ ZIP: 10112  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: Patent Release #1.0, Version #1.25  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/08/323,531  
/ FILING DATE:  
/ CLASSIFICATION: 435  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: US/07/926,784  
/ FILING DATE:  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: White, John P  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: (212)977-9550  
/ TELEFAX: (212)664-0525  
/ TELEX: 422523  
/ INFORMATION FOR SEQ ID NO: 71:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 31 base pairs  
/ TYPE: nucleic acid  
/ STRANDEDNESS: single  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: DNA (genomic)  
/ HYPOTHETICAL: NO  
/ ANTI-SENSE: NO  
/ ORIGINAL SOURCE:  
/ ORGANISM: Synthetic oligonucleotide primer  
/ US-08-323-531-71

Query Match 37.9%; Score 11; DB 1; Length 31;  
Best Local Similarity 42.9%; Pred. No. 1.7e+03;  
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 5 AUNCUCUUNGUAG 18  
DB 20 ATACTTTTCGTAAG 7

RESULT 38  
US-08-198-094-71/C  
/ Sequence 71, Application US/08198094  
/ Patent No. 5741696  
/ GENERAL INFORMATION:  
/ APPLICANT: Cochran Ph.D., Mark D  
/ TITLE OF INVENTION: Recombinant Equine Herpesvirus  
/ NUMBER OF SEQUENCES: 77  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: John P. White  
/ STREET: 30 Rockefeller Plaza  
/ CITY: New York  
/ STATE: New York  
/ COUNTRY: USA  
/ ZIP: 10112  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/198,094  
FILING DATE: February 17, 1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P  
TELEPHONE: (212)977-9550  
TELEFAX: (212)664-0525  
TELEX: 422523  
SEQUENCE CHARACTERISTICS:  
INFORMATION FOR SEQ ID NO: 71:  
LENGTH: 31 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Synthetic oligonucleotide primer  
US-08-198-094-71

Query Match 37.9%; Score 11; DB 1; Length 31;  
Best Local Similarity 42.9%; Pred. No. 1.7e+03;  
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 5 AUNCUNNGUAG 18  
|:|::|:|  
Db 20 ATACTTTCGTAAG 7

RESULT 39  
US-08-480-640A-119/c  
Sequence 119, Application US/08480640A  
Patent No. 603934  
GENERAL INFORMATION:  
APPLICANT: Cochran, Mark D.  
APPLICANT: Junker, David E.  
TITLE OF INVENTION: Recombinant Swinepox Virus  
NUMBER OF SEQUENCES: 225  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: John P. White  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/480,640A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P  
REGISTRATION NUMBER: 28,678  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 278-0400  
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INFORMATION FOR SEQ ID NO: 119:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 31 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Equine Influenza A neuraminidase  
STRAIN: Prague/56  
US-08-480-640A-119

Query Match 37.9%; Score 11; DB 3; Length 31;  
Best Local Similarity 42.9%; Pred. No. 1.7e+03;  
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 5 AUNCUNNGUAG 18  
|:|::|:|  
Db 20 ATACTTTCGTAAG 7

RESULT 40  
US-08-295-802-119/c  
Sequence 119, Application US/08295802  
Patent No. 6127163  
GENERAL INFORMATION:  
APPLICANT: Cochran Ph.D., Mark D  
APPLICANT: Junker M.S., David E  
TITLE OF INVENTION: Recombinant Swinepox Virus  
NUMBER OF SEQUENCES: 188  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: John P. White  
STREET: 30 Rockefeller Plaza  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10112  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/295,802  
FILING DATE: Herewith  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
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TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)977-9550  
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TELEX: 422523  
INFORMATION FOR SEQ ID NO: 119:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 31 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Equine Influenza A neuraminidase  
STRAIN: Prague/56  
US-08-295-802-119

Query Match 37.9%; Score 11; DB 3; Length 31;  
Best Local Similarity 42.9%; Pred. No. 1.7e+03;  
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 5 AUNCUNNGUAG 18  
|:|::|:|  
Db 20 ATACTTTCGTAAG 7

Search completed: April 18, 2004, 09:59:45  
Job time : 50.6667 secs